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C;Species: Bacillus halodurans
C;Pate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: G83753
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4117-4331, 2000
A;Titleic Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                       protease, pyroly
     C.; Siezen, R.J.; Vos,
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R;Voorhorst, W.G.B.; Eggen, R.I.L.; Geerling, A.C.M.; Platteeuw, C.; Siezen, J. 1810. Chem. 271, 20426-20431, 1996
Jaiol. Chem. 271, 20426-20431, 1996
A;Title: Isolation and characterization of the hyperthermostable serine prot A;Reference number: 220481; MUID:96355370; PMID:8702780
A;Recession: T28159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary
A;Status: DxA
A;Status: DxA
A;Status: DxA
A;Cross-references: EMBL,U55835; NID:g1556462; PID:g1556463; PIDN:AAB09761...
A;Experimental source: DSM3638
C;Genetics:
A;Genetics:
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F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                   Indels 136;
                                                                                                                                                                                                                                                  Length 1398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 QVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATE--
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Local Similarity 28.4%; Pred. No. 9.5e-12;
les 129; Conservative 37; Mismatches 153;
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Serine proteinase (EC 3.4.21.-) precursor, extracellular - Xanthomonas campestris pv. c. N.Alternate names: subtilities. Tealated proteinase (S. Serine proteinase (S. Serine proteinase (S. Serine proteinase campestris pv. campestris c. Species : Xanthomonas campestris pv. campestris c. Species : Z1.Nov.1993 #sequence_revision 07-Feb-1997 #text_change 03-Dec-1999 C. Accession: S11890 C. P. S. Dow, U.M.; Daniels, M.J. Mol. Gen. Genet. 220, 433-440, 1990 C. P. P. Dow, U.M.; Daniels, M.J. Mol. Gen. Genet. 220, 433-440, 1990 C. P. P. Dow, U.M.; Daniels, M.J. Mol. Gen. Genet. 220, 433-440, 1990 C. P. P. Dow, U.M.; Daniels, M.J. Mol. Gen. Genet. 220, 433-440, 1990 C. M. Molecule type: DNA A. Reference number: S11890; MUD:90251253; PMID:2187155 A. Molecule type: DNA A. Residues: 1-580 c. LUU.
A. Residues: 1-580 c. LUU.
A. Residues: L-580 c. LUU.
A. Residues: EMBL:X51635; NID:948533; PIDN:CAA35962.1; PID:948534 A. Molecule type: DNA A. Residues: DNA A. Residues: EMBL:X51635; NID:948533; PIDN:CAA35962.1; PID:948534 A. Molecule type: DNA A. Residues: L-580 c. LUU.
C. Superfamily: subtilisin, subtilisin homology carine proteinase F. J. S2D Domain: signal sequence #status predicted cs1Gs c. F. J. Domain: subtilisin homology c. SET.
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                                                                                                                                                                                                                                                       DPNG----HGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTL--FSQA
                                                                                                                                                                                                                                                                                                                                                                                       118 WNAGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ENYRPSFGSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 AISVGATRLPYNKYKASVFTSDGIDYPSADIMGFPSDEELLELDGETYEYAFAGLGKPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEGVDVECKIALIVRGEIPFVEKAENAKAAGAVGAIIYNNVAGVQPTVPGLAIPTIMLSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     514 IPTHOPDDPY--GYGSRO----GTSMASPHVAGAAALLLEAH-PNWGV----DHVKAALM
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                                                                                                                                                                                                                                                                                                 AGATDV----GLGYPSGDQGWGRVTLDKSLNVAYVNEATALAT---------
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                                                                 Gaps
                                                                                                                           GLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGR-----TNN---
                                                             265;
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   Length
                                                                 Indels
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13.4%; Score 302.5; DB 2;
.larity 24.0%; Pred. No. 6.5e-12;
Conservative 57; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 298.5; DB 2
Pred. No. 7.6e-12;
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Best Local Similarity
                                  Best Local Similarity
Matches 150; Conserv
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DD 607 LVITAGASTLANDTRINGTRANDEVIPPSSRGPTGGGYPKPDIVNIGAF	A;Cross-references DBBJ;DB660, NID:g1536787; PIDN:BAA18912.1; PID:d1019647; PID:g12160 A;Speriments active extain 0-7 C;Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sens C;Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sens C;Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sens C;Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sens C;Comment: This enzyme belongs to class I send to be class I send to send t
Matches 137; Conservative 51; Mismatches 149; Indels 135; Gaps 26;	RESULT 9 TEACULT 9 TEACULT 9 TEACH CALCE AND THE ALVER CARDED PROTEINAGE - Staphylothermus marinus N.A.Lerande names: Myperthermus marinus C.Species: Staphylothermus R.Species: T.2000 R.State: December: Z.20559; WID: 938442; PRID: 8793300 A.State: December: Z.20559; WID: 9388442; PRID: 9374756; PIDN: AAB02323.1 A.State: December: Z.20559; WID: 9388442; PRID: 9374756; PIDN: AAB02323.1 A.State: December: Z.20559; WID: 9388442; PRID: 9374756; PIDN: AAB02323.1 A.State: December: Z.20559; WID: 9374755; PID: 9374756; PIDN: AAB02323.1 A.State: December: Z.20559; WID: 9388442; PRID: 9374756; PIDN: AAB02323.1 A.State: December: Z.20559; WID: 9388442; PRID: 9374756; PIDN: AAB02323.1 A.State: December: Z.20559; WID: 9388442; PRID: 93884442; PRID: 93884442; PRID: 938844445; PRID: 938844445; PRID: 93884445; PRID: 938844445; PRID: 938844445; PRID: 938844445; PRID: 93884445; PRID: 938844445; PRID: 938844445; PRID: 938844445; PRID: 938844445; PRID: 938844445; PRID: 938844445; PRID: 93884445; PRID: 938844445; PRID: 938844446; PRID: 938844446; PRID: 938844446; PRID: 938844446; PRID: 938844446; PRID: 938844446; PRID:

Qy 264 VAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYPSGDQGWGRVTLDKSLNVAYVNEA 323	Db 322 LNGTSMATPHVAGAAALVKQKNPSWSNVQIRNH-LKNTATSLGSTNL 367
DD 448 AALIKQAAKPSATPDEVETILKNTTRSFAGSCSNCGTGVVDAAAAVNEA 495	Qy 298 GYPSG 302
QY 324TALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTASYT 362	Db 368 -YGSG 371
363 LVNDLDLVITAPNGGKYVGNDFSYPYDNNWDGRNNVENVFINAPGSGTYTIEV 41 S42 MSGGTGADLVYXLGSOPISSSYPCRFYGGRAFVGSFDAPOAGTYFYNI 59	RESULT 12 JS0173 alkaline proteinase (EC 3.4.21) A precursor - Vibrio alginolyticus N.Alternate names: alkaline serine exporoteinase A
416 QAYNVPSG 423	ep-199
DD S92 NGKKAYSG 599 RESULT 11 A49778 A101 Precursor - Bacillus alcalophilus (strain	Ribeane, S.M.; Robb, F.T.; Robb, S.M.; woods, D.K. Gene 76, 281-288, 1989 A.Title: Nucleotide sequence of the Vibrio alginolyticus calcium-dependent, detergent-r A;Reference number: JS0173; MUID:89326126; PMID:2546861 A;Molecule type: DNA
0002	A;Residues: 1-534 <dea> A;Cross-references: GB:M25499; NID:g155250; PIDN:AAA27550.1; PID:g155251 C;Comment: This protein is a calcium-dependent and sodium dodecyl sulfate-resistant pro C;Superfamily: subtilisin; subtilisin homology</dea>
R; van der Laan, J.C.; Gerritse, G.; Mulleners, L.J.S.M.; van der Hoek, R.A.C.; Quax, W.J. Appl. Environ. Miscobiol. 57, 901-909, 1991 A; Title: Cloning, characterization, and multiple chromosomal integration of a Bacillus a A; Reference number: A49778; MUID:91282483; PMID:2059048 A; Accession: A49778 A; Molecule type: DNA	C; Keywords: calcium; hydrolase; serine proteinase F;1-21/Domain: signal sequence #status predicted <sig> F;22-534/Product: alkaline serine proteinase A #status predicted <wat> F;171-378/Domain: subtilisin homology <sbt> F;171-273-297-299/Region: SI specificity crevice #status predicted F;180,213,363/Active site: Asp, His, Ser #status predicted</sbt></wat></sig>
	7%; Score 265; DB 3%; Pred. No. 1e-0
Aono, R.; Horiko structural gene f	**************************************
A;Accession: JC1244 A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: J-380 <tak> A;Molecule type: J-380 <tak< <tak<="" <tak<<="" a;molecule="" j-380="" td="" type:=""><td>٠</td></tak<></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak></tak>	٠
A.Experimental Source: Garillus alcalophilus Vedder, ATCC 21522 (Bacillus sp. 221) C.Superfamily: subtilisin, subtilisin homology C.Keywords: hydrolase; serine proteinase; zymogen	104 GGLESVAGILE VENERLASSELNGRGILLVAG I IGGGEL - GYAKAN MENGYEN EN E
Fil-27/Domain: signal sequence #status predicted <sig> Fil8-11/Domain: activation peptide #status predicted <pro> Fil28-11/Domain: activation peptide #status predicted <pro> Fil13-380/Product: alkaline serine proteinase #status predicted <pri> Fil34-340/Domain: subtilisin homology <sbi> Fil43,173,326/Active site: Asp, His, Ser #status predicted</sbi></pri></pro></pro></sig>	Db 249 SGVIAGVDMVAANASGPSVANMSIGGGQSVALDSAVQSG-VSFMLAAGNSN 302 Qy 164 PNSGTISAPGTAKNAITVGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPG 223 16
Query Match 11.9%; Score 269; DB 2; Length 380; Best Local Similarity 31.8%; Pred. No. 3.5e-10; Matches 97; Conservative 35; Mismatches 99; Indels 74; Gaps 14;	QY 224 TFILSARSSLAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSL 283 1
OY 13 AQNNYGLYQGQYVAVADIGLDIGRNDSSMHEAFRGKITALYALGRINNANDBNGHGTHV 72	QY 284 IKAALIAGATDVGLGYPSGDQGWGRVTLDKSLNVAY 319 :: ::
QY 73 AGSVLGNALN-KGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNAGARIHTNSW 129	Qy 320 VNEATALATGGKATYSFQAQAGKPLKISLVWTDAPGSTTASYTLVNDLDLVTAPNGGKX 379
QY 130 GAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATENYRP 189	QY 380 VGNDFSYPYDNNWDGRNNVENVFINAPQSGTYTIEVQAYNVPSG 423
FGSLADNPN DQNN GGTSMATPI	Bacillus sp. (strain TA39)
	C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jun-1999

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probable surface layer-associated STABLE proteinase APE0607 - Aeropyrum pernix (strain probable surface layer-associated STABLE proteinase APE0607 - Aeropyrum pernix
C.Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C.Accession: A72647
B.Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
A.Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A.Reference number: A72450; MUID:99310339; PMID:10382966
A.Scatus: preliminary
A.Status: preliminary
A.Status: Drahamary
A.Status: Drahamary
A.Status: L-1331 < KAM>A.Status: DNA
A.Status: DNA
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                                                                                                                                                                                                                                                                                                                                  130 GAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATENYRP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 SFGSLADNPNHIAQFSSRGATRDG-----RIKPDVTAPGTFILSARSSLAPDSSFWANY 243
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479 GYIETSLRGVAPGAKI-----AAGGSFLINVFVAQLFLSGFEPQDSPLNWVYTGEHQV 531
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                                                    GOGOVVAVADTGLDTGRNDSSMH-EAFRGKITALYALGRT---NNANDPNGHGTHVAGSV
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C;Species: Bacillus sp.
C;Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999
C;Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999
C;Accession: S25893
R;Davail, S; Feller, G; Narinx, E; Gerday, C.
Gene 119, 143-144, 1992
A;Title: Sequence for the subtilisin-encoding gene from an antarctic psychrotroph Bacil
A;Reference number: S25835, MUID:93012966; PMID:1398082
A;Title: Sequence 125835, MUID:93012966; PMID:1398082
A;Residues: 1-419 c.DAV.
A;Residues: 1-419 c.DAV.
A;Residues: 1-419 c.DAV.
C;Superfamily: subtilisin, bubtilisin, homology
C;Reywords: extracellular protein; hydrolase; serine proteinase
F;11-23/Domain: signal sequence #status predicted c.SIG.
F;111-419/Product: microbial serine proteinase #status predicted
F;135-373/Domain: subtilisin homology c.SET.
F;144,184,359/Active site: Asp, His, Ser #status predicted
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C; Accession: $23407

R; Marinx, E.; Davall, S.; Feller, G.; Gerday, C.

Biochim. Biophys. Acta 1131, 111-113, 1992

A; Title: Nucleotide and derived amino acid sequence of the subtilisin from the A; Reference number: $23407; MUID:92256481; PMID:1581352

A; Recession: $23407; MUID:92256481; PMID:1581352

A; Recession: $23407; MUID:92256481; PMID:1581352

A; Residues: 1-420 cNAR>

A; Residues: 1-420 cNAR>

A; Residues: 1-420 cNAR>

A; Genetics:
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11.7%; Score 263.5; DB 1; Length 420;
Best Local Similarity 29.0%; Pred. No. 9.2e-10;
Matches 92; Conservative 46; Mismatches 120; Indels 59; Gaps
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Best Local S.
Matches 81
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Search completed: March 31, 2004, 16:10:20 Job time : 12.3246 secs

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Mismatches:
Indels:
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Matches:
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                            LOCATION: 338...2539
IDENTIFICATION METHOD:
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                9.190-25
345.50
41.15%
29.20%
15.29%
                NAME/KEY:
                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-514-340-3
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GENE ENCOING A PROTEIN HAVING ASYMMETRIC
HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE
ITS EXPRESSION PRODUCT
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ATCGCCGACCCGGTCTCGGTGAGCTTCGGCGTCCAGCAGTGGCCGCACACGACGACGAG
                                                                                                 364
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                                                                                                 SerLeuValTrpThrAspAlaProGlySerThrThrAlaSer-----TyrThrLeuVal
                                                                                                                                                                                             GlnLysAlaThrTyrSerPheGlnAlaGlnAlaGlyLysProLeuLysIle
                                                                .898 CCGGTCACCAAGCAGCTGACCTACCGCAACCTCGGCACCCCAGGACGTCACGCTGAAGCTG
                                                                                                                                                                                                                                                                                                     AsnValPheIleAsnAlaProGlnSerGlyThrTyrIle-----
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STREET: 2033 K Street, N.W., #800
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/514,340
FLING DATE: 28-Feb-2000
CLASSIFICATION: <URKNOWN:
APPLICATION WUMBER: 09/000,016
FILING DATE: January 30, 1998
ATTORNEY/AGENT INPORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REGISTRATION NUMBER: 40,949
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
STRAIN: Streptomyces viridosporus
STRAIN: A-914
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2539 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09514340 Patent No. 6361987 GENERAL INFORMATION:
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STRANDEDNESS: double
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TITLE OF INVENTION: GENE
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CITY: Washington
STATE: D.C.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                           ORGANISM: Streptomyces viridosporus
STRAIN: A-914
                                                                                                                                                                                                                                                                                                     ORGANISM: Streptomyces antibioticus
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2809 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
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IDENTIFICATION METHOD:
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Best Local Similarity:
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ORIGINAL SOURCE
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NAME/KEY:
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DB:
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Sequence 1, Application US/09000016
Sequence No. 6143541
GENERAL INFORMATION:
APPLICANT: AAKITA ARISAWA et al.
APPLICANT: AAKITA ARISAWA et al.
TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DERIV
TITLE OF INVENTION: ITS EXPRESSION PRODUCT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2047
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                                                                                                                                                          1898 CCGGTCACCAAGCTGACCTACCGCAACCTCGGCACCCAGGACGTCACGTGAAGCTG 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1958 ACGICGACCGCCACCAACCCCAAGGCAAGGCGGCCCCGGCGGGCTICTICACGCTGGGC 2017
                                                                                                                                                                                                                                                                                      1838 ATCGCCGACCCGGTCTCGGTGAGCTTCGGCGTCCAGCAGTGGCCGCACACCGGACGACGAG 1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                      347 SerLeuValTrpThrAspAlaProGlySerThrThrAlaSer-----TyrThrLeuVal 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 SerTyrProTyrAspAsnAsnTrpAspGlyArg-------AsnAsnValGlu 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 AsnAspLeuAspLeuVallleThrAlaProAsnGlyGlnLysTyrValGlyAsnAspPhe 384
                                                                                                                         ProAsnGlyAspGlnGlyTrpGlyArgValThrLeuAsnLysSerLeuAsnValAlaTyr 319
                                                                                                                                                                                                                                                                                                                                               -----GlnLysAlaThrTyrSerPheGlnAlaGlnAlaGlyLyBProLeuLysIle 346
              ---IlealaGlyAlaThrAspValGlyLeuGlyTyr 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2048 AGCGCCTCCGTCGACATGACCGCCGACACCCGGCTCGGCGGCGCGCGTGGACGGCGCGTAC
                                                  320 ValAsnGluAlaThrAlaLeuAlaThrGly-------------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Wenderoth, Lind & Ponack, L.L.P. 2033 K Street, N.W., #800
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MEDIUM TYPE: Diskette, 3.5 inch, 1.4
COMPUTER: Diskette, 3.5 inch, 1.4
COMPUTER: IBM Compatible
OFBRATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,016
FILING DATE: January 30, 1998
CLASSIFICATION NUMBER: US/09/000
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
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NAME: Warren M. Cheek, Jr.
REGIENGATION UNDRER: 33,867
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-820
TELEPAX: 202-721-825
                    LeulleLysAlaAlaLeu----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C. COUNTRY: U.S.A.
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STREET: 2033 K St
CITY: Washington
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US-09-000-016-1
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Percent Similarity: 41.15% Conservative: 54 Best Local Similarity: 29.20% Mismatches: 170 Query Match: 15.29% Indels: 96 DB: 3 Gaps: 16	US-09-985-689A-4 (1-433) x US-09-000-016-3 (1-2539)	Qy 18 GlybeuTyrGlyGlnGlyGlnValValAlaValAlaAspThrGlybeuAspThrGlyArg 37	Db 998 GCTACGACGACGACGACGACGATCGCCGTCCTGGACACGACTCGACACGAGC 1054	Qy 38 AsnAspSerSerMetHisGluAlaPheArgGlyLys1leThrAlaLeuTyrAlaLeuGly 57		AlaGlyserValLeu 77 	Db 1100 GCCGCGCCCGGCGCCGACAAGGTGGGCCACGGCACCCACGTCGCCTCGATCGCGGCG 1159	Oy 78 GlyAsnAlaLeuAsn	Db 1160 ĠĠĊacggggggggggggggggggggggggggggggggggg	Qy 93 PheGlnSerIleMetAspSerSerGlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThr 112	113 LeuPheSerGlnAlaTrpAsnAlaGlyAla	 	Qy 131 Ala	Db 1328 GGCATGGACACCGGAGACCGGCTGGAGGCGGCG	luTyrValArgAsnAsnAspM	Db 1367 GTCGACAAGCTGTCCGCCGAGAAGGGGGGTCCTGTTCGCCATCGCGGCCGAACGAGGGC 1426	ProasnSerGlyThrileSerAlaFroGlyThrAlaLysAsnAlaileThrValGlyAla 183	1427 CCGGAGTCG		204 PheSerSerArgGlyAlaThrArgAspGl	rccc 15	223 GlyThrPheIleLeuSerAlaArgSerSerLeuAlaProAspSerSerPheTrpAlaAsn 2	TOHO TOO	243 TyrAsnSerLysTyrAlaTyrMetGlyGlyThrSerMetAlaThrProlleValAlaGly		PhelleLysAsnArgGlylleThrProLysProSer 282		VLeuGlyTyr	· U	Qy 300 ProAsnGlyAspGlnGlyTrpGlyArgValThrLeuAsnLysSerLeuAsnValAlaTyr 319	18	Qy 320 ValAsnGluAlaThrAlaLeuAlaThrGly329
Oy 358 ThrAlaSerTyrThrLeuValAsnAspLeuAspLeuVallleThrAlaProAsnGlyGln 377	Oy 378 LysTyrValGlyAsnAspPheSerTyrProTyrAspAsnAsnTrpAspGlyArgAsnAsn 397	Db 1465GGGAACGAGGTTGACTACTACACCGCCTACTACGGC 1503	Oy 398 ValgiuAsnValPheileAsnAlaProGlnSerGlyThrTyrileIleGluValGlnAla 417	Db 1504 TTCGAGAAGGTCGGCTACTACAACCGGCGGGAACCTGGACGGTCAAGGTCGAGGTCGAGG 1563	Qy 418 TyrAsnValProSerGlyProGlnArgPheSerLeuAlaIleVal 432	Db 1564 TACAAGGGCGCGCGAACTACCAGGTCGTC 1599	RESULT 12	US-09-000-016-3 Sequence 3, Application US/09000016 ; Datent No. 6443441	GENERAL INFORMATION:	; APPLICANT: Akira ARISAWA et al.; ; TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC; ; TITLE OF INVENTION: HYDROLASE ACTIVITY ENCETTUTED 1,4-DIHYDROPYRIDINE DERIV TITLE OF INVENTION: 1TS EXPERSATION PRODUCT	NUMBER OF INDUSTRY	STREET: 2033 K Street, N.W., #800	ington	COUNTRY: U.S.A.	EE	COMPUTER: IBM Compatible COPERATING SYSTEM: MS-DOS	; SOFTWARE: Wordperfect 5.1 ; CURENT APPLICATION DATA: ; abblication winders : 15/00/000 016	ry 30, 1998	; PRIOR APPLICATION DATA; ; APPLICATION NUMBER: STITM DAME.	riling Dair: ATTORNEY/AGENT INFORMATION: NAME: Warren M. Cheek, Jr.	; REGISTRATION NUMBER: 33,367 ; REFERENCE/DOCKET NUMBER:	; TELECOMODICATION THOUGHATION: ; TELEPHONE: 202-721-8200 ; TELEPAX: 202-721-8250	TINDORMATION BOS SEO ID NO. 3.	ACTERISTICS:	nucleic acid	TOPOLOGY: linear work of the w	E:	; ORKANISM: Streptomyces viridosporus ; STRAIN: A-914 posyming	CDS) LOCATION: 3582539 ; IDENTIFICATION METHOD: E	0.040	Alignment Scores: Pred. No.: 9.19e-25 Length: 2539 Score: 345.50 Matches: 132

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321 decanacreacerechedederecerecesacangangedededededecriteae 1380
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                                                                                                                                                                                                                                                                                                                                             913 TACACCGTCGGCTCACCGCGCGCGAGAGGTCATAACCGTCGGTGCA----- 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         964 ----------GTTGACAGCAACGACAACATCGCCAGCTTCTCCAGC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 ArgGlyAlaThrArgAspGlyArgIleLy8ProAspValThrAlaProGlyThrPheile 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 AspGlnGlyTrpGlyArgValThrLeuAsnLysSerLeuAsnValAlaTyrValAsnGlu 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 AlathralaLeuAlathrGlyGln-------bysAlathrTyrSerPheGln 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaginAlagiyLysProLeuLyslieSerLeuValfrpThrAspAlaProGlySerThr 357
                                                                                                                                                                                                                                                              AlaAsnLeuValPheGlnSerIleMet-----AapSerSerGlyGlyLeuGlyGlyLeu 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 GlythrileSerAlaProGlyThrAlaLysAsnAlaIleThrValGlyAlaThrGluAsn 186
                                               613 TCAATAGCAGCTGSTACTGGAGCAGCAAGTAATGGCAAGTACAAGGGAATGGCTCCAGGA 672
                                                                                                                                                                                                      74 GlyservalLeuGly------AsnAlaLeuAsnLysGlyMetAlaProGln 88
                                                                                                                                                                                                                                                                                673 GCTAAGCTGGGAAATTAAGGTTCTAGGTGCCGATGGTTCTGGAAGCATATCTACTATA
                                                                                                                                                                                                                                                                                                                                                                               127 AsnSerTrpGlyAlaProValAsnGlyAlaTyrThrAlaAsnSerArgGlnValAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 TyrvalargasnasnaspMetThrvalLeuPheAlaalaglyAsnGluGlyProAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853 AACGCCTGGGACGCCGGTATAGTAGTCTGCGTCGCCGCCGGCAACAGCGGGCCGAACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 TyrArgProSerPheGlySerIleAlaAspAsnProAsnHisileAlaGlnPheSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 LeuArgGluHisPhelleLysAsnArgGlyIleThrPro------LysProSerLeu
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TTTGTCAATGGTAGG---AGTTATCCATACGATGACCATGGACATGGAACTCATGTAGCT
                                                                                                                                             54 ТугАlaLeuGlyArgThrAsnAsnAlaSerAspProAsnGlyHisGlyThrHisValAla
                            16 AsnTyrGlyLeuTyrGlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThr
                                                                                   GlyArgAsnAspSerSerMetHisGluAlaPheArgGlyLysIleThrAlaLeu-----
US-09-985-689A-4 (1-433) x US-08-894-818B-6 (1-1977)
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                                               ---ACCGCCTACTATGGA 1503
                                                                                            398 ValGluAsnValPhelleAsnAlaProGlnSerGlyThrTyrIleIleGluValGlnAla 417
                  LysTyrValGlyAsnAspPheSerTyrProTyrAspAsnAsnTrpAspGlyArgAsnAsn 397
                                                                                                                                                                1564 TAC-----AGCGGAAGTGCAAACTATCAAGTAGATGTGGTA 1599
                                                                                                                                  TyrAsnValProSerGlyProGlnArgPheSerLeuAlaIleVal 432
                                                                                                                                                                                                                                                             APPLICANT: TAKAKURA, Hikaru
APPLICANT: TAKAKURA, Mio
APPLICANT: NORISHITA, Mio
APPLICANT: MITTA, Masanori
APPLICANT: MITTA, Masanori
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUNASAWA, Susumu
APPLICANT: TSUNASAWA, Susumu
APPLICANT: TATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1977
129
63
172
71
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CAGGTT-----GACTACTCTTAC----
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                                                                                                                                                                                                                     Sequence 6, Application US/08894818B
Patent No. 6261822
GENERAL INFORMATION
APPLICANT: TAKAKUZA, Hikaru
APPLICANT: MORISHITA, Mio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET UNBER: TAKA
TELECOMMULICATION INFORMATION:
TELEPHONE: (202) 737-3528
INFORMATION FOR SEQ 10 No: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1977 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: genomic DNA
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395.50
44.14%
29.66%
17.50%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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US-08-894-818B-6
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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 31, 2004, 15:58:03; Search time 7.49423 Seconds (without alignments) 3008.498 Million cell updates/sec Run on:

US-09-985-689A-5 2261 1 NDVARGIVKADVAQNNYGLY........EVQAYNVPSGPQRFSLAIVH 433 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	ription	dictyos	dictyostel	bacillu	pyrococ	P23314 xanthomonas	bacillus	P29600 bacillus le	bacillus	bacillus	vibrio al	bacillus	bacillus	bacillus	bacillus	streptoco	bacillus	bacillus		P08594 thermus agu		P58099 streptococc	P29118 cephalospor	O14703 homo sapien	P11018 bacillus su	cricetu		ratto	bacillu	bacillus	bacillu	bacillus	bacill	bacil
SUMMARIES	ID	c picp	TAGB_DICDI	SUBV_BACSU	PLS PYRFU	EXPR XANCP	PRTM_BACSP	SUBS_BACLE	ELYA_BACAO	ELYA_BACCS	PROA_VIBAL	SUBT_BACS9	SUBB_BACLE	THES_BACSP	WPRA BACSU	SCA1_STRPY	ELYA_BACSP	SUBT_BACLI	ISP BACCS	AQLI THEAQ	TKSU_PYRKO	SCA2_STRPY	ALP_CEPAC	MS1P_HUMAN	ISP1_BACSU	MS1P_CRIGR	MS1P_MOUSE	MS1P RAT	SUBN_BACNA		SUBT_BACST	ű	B	SUBT_BACAM
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P07518 bacillus ju P00781 bacillus li P04072 thermoactin P42780 bacteroides C9778 magnaporthe P29138 metarhizium P29139 paenibacill Q03420 trichoderma P33295 aspergillus P40903 schizosacch Q9uts0 schizosacch P29143 halophilic
SUBT BACPU SUBD_BACLI BRET THEVU BPRX BACNO SMP1_MAGPO CUPP METAN ISP PREPO ALP TRIHA ISPE ASPNG ISPE ASPNG ISPE ASPNG ISPE ASPNG ISPE SCHPO XLP1 SCHPO HLY HAL17
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## ALIGNMENTS

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MEDLINE=95262903; PubMed=7744252;
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27.7%; Pred. No. 9.9e-25;
Live 77; Mismatches 158; Indels 190; Gaps 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                              274 NRGITPKPSLIKAALIAGA-----TDVGLGYPSGD-------QGWGRVTLD 312 ; ; | | | | | | | | | : : | | | | | | : :
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POLY-GLY.
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POLY-ASP.
POLY-ASN.
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POLY-ASN.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its world; the institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a long as entry of your former or sentities requires a long as a commercial content and the commercial content and an email to license@isb-sib.ch).
                                                                       727 NWLHVVNNNNSNNNNKTSDGITKFDGIGGLDLRLVKPNQWKEESLSTGQNTSYCFTYKPS 786
                                                                                                                                                       337 --QAQAGKPLK---ISLVWTDAPGSTTASYTLVNDLDLVITAPNGQKYVGNDFSYPYDN- 390
                                                                                                                                                                                                                 787 SSSSNSGNNIPRVVATLVWTDPPSYAGAKFNLVNNLDLTMI-----YYRDNGSTIFYSNQ 841
313 KSLNVAYVNEAT-------336
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DR PIR; TU8267; TU8267.

MERCPES, 508.UPW; -.

DR InterPro; IPR001964; tagB.

DR InterPro; IPR001496; AAA_ATPasse.

DR InterPro; IPR001499; ABC_transporter.

DR InterPro; IPR002499; ABC_transporter.

DR Pfam; PF000664; ABC_transporter.

DR Pfam; PF000665; Peptidase_S8.

DR Pfam; PF000065; ABC_trans.

DR Pfam; PF000065; ABC_trans.

DR Pfam; PF000065; ABC_trans.

DR Pfam; PF000065; ABC_transporter; 1.

DR PROSTIE; PS00123; SUBTILISE_R1; 1.

DR PROSTIE; PS00124; ABC_TRANSPORTER 1; 1.

DR PROSTIE; PS00126; SUBTILASE_ARP; FALSE_NEG.

DR PROSTIE; PS00136; SUBTILASE_ARP; TALSE_NEG.

DR PROSTIE; PS00137; SUBTILASE_ARP; TALSE_NEG.

DR PROSTIE; PS00136; SUBTILASE_ARP; TALSE_NEG.

DR PROSTIE; PS00136; SUBTILASE_SER; 1.

KW Hydrolase; Serine protesse; ATP-binding; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shaulsky G., Kuspa A., Loomis W.F.;
"A multidrug resistance transporter/serine protease gene is required
for prestalk specialization in Dictyostelium.";
Genes Dev. 9:1111-1122(1995).
-:- FUNCTION: Intercellular communication via tagh may mediate
integration of cellular differentiation with morphogenesis.
-:- SIMILARITY: In the N-terminal section; belongs to peptidase family
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-!- SIMILARITY: STRONG, TO TAGC.
                                                                                                                                                                                                                                                                                                                                                                     842 GGSSFLGLAPTQDTLNNVEGIVHNPTEPMTREMVAGTNVPMGPQNFS 889
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01-OCT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Prestalk-specific protein tagB precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
NCBI_TaxID=44689;
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P-LKISLVWIDAPGSTTASYTLVNDLDL-----VITAPN--GOXYVGNDFSYPYDN 390
     MEDILALE SUGGESTION OF THE STATE OF THE STAT
                                                                                                     PRIVATLYWTDPPSYSGAKFNLVNNLDLLLLNSDDDSIITIGNSGGSLQPAGKVAQQP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 161-195.
MEDLINE=92041574; PubMed=1938892;
Sloma_A., Rufo G.A. Jr., Theriault K.A., Dwyer M., Wilson S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and characterization of the gene for an additional extracellular serine protease of Bacilius subtilis."; J. Bacteriol. 173:6889-6895(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4.21.-).
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                                                                                                                                                                                                   --DILINIVEGIIINPIKAMNYKFTIAGTNVPIGPQKPS 938
                                                                                                                                                                         391 NWDGRNNVENVFINAPQSGTYTIEVQAYNVPSGPQRFS
                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
110-CCT-2003 (Rel. 42, Last annotation update)
Minor extracellular protease vpr precursor (EC
Bacillus subtilis.
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519 HDPDHPY--GYGSKQ----GTSMASPHIAGAVAVIKQ---
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                                                                                                        620 NETFTIENQSSIRKSYTL-
                                                                                                                                   406 POSGTYTIEVO 416
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659 HQTGKATAKVK 669
                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                     Pyrococcus furiosus
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                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWEL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 AVQDGADVMNLSLGNSLNNPDWATSTALD-WAMSEGVVAVTSNGNSGPNGWTVGSPGTSR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------NHIAQFSSRGATRD-GRIKPDVTAPGTFILSARSS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSL--IKAALIA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NANDPNG----HGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AWNAGARIHTINSWGAPVNGAYTANSRQVDEYVRINDMTVLFAAGNEGFNSGTISAPGTAK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAISVGATQIPLNEYAVIFGSYSSAKVMGYNKEDDVKALNNKEVELVEAGIGEAKDFEGK 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NDSSMHEAFRGKITALYALGRTN
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(BY SIMILARITY).

(BY SIMILARITY).
                                               Nature 390:249-256(1997).

Nature 390:249-256(1997).

-I FUNCTION: NOT REQUIRED FOR GROWTH OR SPORULATION.

-I SUBCELLULAR LOCATION: Secreted.

-I FTM: PROBABLY UNDERGOES C-TERMINAL PROCESSING OR PROTECLYSIS.

-I SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                          Interro, 120022; PA; 1.
Pfam; PF0222; PA; 1.
Pfam; PF00082; Peptidase S8; 1.
PRINTS; PR00123; SUBTILIASE ASP; 1.
PROSITE; PS00134; SUBTILIASE ASP; 1.
PROSITE; PS00137; SUBTILIASE BIS; 1.
PROSITE; PS00138; SUBTILIASE SER; 1.
Hydrolase; Serine protease; Zymogen; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.8%; Score 312; DB 1; Length 806; 23.4%; Pred. No. 6.7é-13; ive 56; Mismatches 156; Indels 210;
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(1) P984E3BF0B66GDDD CR(1)
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                                                                                                                                                                                                                                                                                                              Subtilist; BG10591; vpr.
InterPro; IPR003137; PA.
InterPro; IPR003209; Peptidase SB.
InterPro; IPR0090209; Protease_Inhib.
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EMBL; X73124; CAA51601.1; -.
EMBL; Z99123; CAB15835.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161
189
233
534
534
806 AA;
                                                                                                                                                                                                                                                                         PIR; A41341; A41341
HSSP; P00782; 2SBT.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                      619
                                                                                                                                                                              405
----AKPKWSVEQIKAAIMN 565
                                                                                                                                                                                                                                         ------EYSFNGSGISTSGTSRVVIPA 658
                                                       291 GATDV----GLGYPSGDQGWGRVTLDKSLNVAYVNEATALATGQKATY-SFQAQAGKPLK
                                                                                                               566 TAVTLKDSDGEVYPHNAQGAG-----SARIMNAIKADSLVSPGSYSYGTFLKENGNETK
                                                                                                                                                                              346 ISLVWTDAPGSTTASYTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINA
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the hyperthermophilic archaeon
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-!- MISCELLANEOUS: Thermostable, high activity at 95 degrees Celsius.
-!- SIMILARITY: Belongs to peptidase family 58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROW N.A., SEQUENCE OF 150-184, AND CHARACTERIZATION.
STRAIN-VCI / DSM 3638 / ATCC 43587 / JCM 8422;
MEDLINE-96355370; PubMed=8702780;
Voorhorst W.G.B., Eggen R.I.L., Geerling A.C.M., Platteeuw C.,
Siezen R.J., de Vos W.M.,
"Isolation and characterization of the hyperthermostable serine
protease, pyrolysh, and its gene from the hyperthermophilic ar
Pyrococus furiosus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb P.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Pyrolysin procursor (EC 3.4.21.-).
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pathovar campestris.";
Mol. Gen. Genet. 220:433-440(1990)
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P23314;
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                                                                                                     PRINTS; PR0723; SUBTILISIN.
PROSITE; PS00134; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_HIS; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Complete proteome.
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Pfam; PF00082; Peptidase_S8; 1.
Pfam; PF04151; PPC; 1.
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RAIN-ATCC 33913 / NCPPB 528;

RAIN-ATCC 33913 / NCPPB 528;

RAIN-ATCC 33913 / NCPPB 528;

REDLINE=20202145; PubMed=12024217;

RA SILVA A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan D.R.,

A Quagglo R.B., Monteiro-Vitorello C.B., Van Sluya M.A., Almeida N.F.,

A Alves L.M.C., do Amaral A.M., Destrolini M.C., Camargo L.B.A.,

RA Alves L.M.C., do Amaral A.M., Destrolini M.C., Camargo L.B.A.,

RA Alves L.M.C., Coutnho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Alves L.M. Rishi L.T., Leite R.C.C., Ferro M.I.T.,

RA Estuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Estuyama A.M., Nachado M.A., Madaira A.M.B.M., Martinez-Rossi N.M.,

Martine E.C., Maidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Schubal J.C., Kitajima J.P.,

Romparison of the genomes of two Xanthomonas pathogens with differing

R. Spinola L.A.F. Takita M.B., Tamura R.E., Teixeira E.C.,

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                                                           GLGYPSGDQGWGRVTLDKGLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPG 355
NYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGAT-----DV
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Liu Y.-N., Tardy J.-L., Clarke B.R., Dow J.M., Daniels M.J.;
"A multipurpose broad host range cloning vector and its use to
characterise an extracellular protease gene of Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas campestris (pv. campestris).Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;Xanthomonadaceae; Xanthomonas.
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01-NOV-1991 (Rel. 20, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Extracellular protease precursor (EC 3.4.21.-)

    -!- SIMILARITY: Belongs to peptidase family S8.

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MEDITIES 953 8832; MUDDEGE-63337; MEDITIES 9538812; MUDDEGE-63337; MEDITIES 9538812; MEDITIES 9538812; MEDITIES 9538812; MEDITIES 9538812; MEDITIES 9538813; MEDITIES 953813; ME
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   "Structure of a new alkaline serine protease (M-protease)
Bacillus sp. KSM-K16.";
Acta Crystallogr. D 51:199-206(1995).
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InterPro; IPR000209; Peptidase_S8.
InterPro; IPR007280; PPC.
InterPro; IPR009020; Protease_inhib.
Pfam; PF00082; Peptidase_S8; 1.
Pfam; PF04151; PPC; 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILIASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_ASP; 1.
PROSITE; PS00138; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_ER; 1.
Hydrolase; Serine Procease; Zymogen; Signal; Complete proteome.
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01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
M-protaes (EC 3.4.21...)
Bacillus sp. (strain KSM-K16).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Yamane T., Kani T., Hatanaka T., Suzuki A., Ashida T.,
Kobayashi T., Ito S., Yamashita O.;
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                                                                                                                                                                                                                                                               -----DONNNRASFSQYGAGL-----DIVAPGVNVQSTYP------GSTYAS 210
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                                                                                                                                                        73 AGSV--LGNALN-KGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNAGARIHTNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 37:13446-13452 (1998).

-!- FUNCTION: Subtilisin is an extracellular alkaline serine protease, it catalyzes the hydrolysis of proteins and peptide amides.

-!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity for peptide bonds, and a preference for a large uncharged residue
                                                                                                                                  15 AAHNRGLTGSGVKVAVLDTGIST-----HPDLNIRGGASFVPGEP-STQDGNGHGTHV
                                                                                                                                                                                                                AQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRINNANDPNGHGTHV
                                                                                                                                                                                                                                                                                  250 MGGISMATPIVAGNVA------QLREHFIKNRGITPKPSLIKAALIAGATDVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   structure of the alkaline proteinase Savinase from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR.
MEDLINE=96184541; PubMed=8654411;
MEDLINE=96184541; PubMed=8654411;
MEDLINE=96184541; Pepermans H.A.M.; Hilbers C.W., van de Ven F.J.M.;
"Backbone dynamics of the 269-residue protease Savinase determined from 15N-NMR relaxation measurements.";
Eur. J. Blochem. 235:629-640(1996).
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MEDLINE=99426039; PubMed=9753430;
Kuhn P., Koapp M., Soliis S.M., Ganshaw G., Thoene M., Bott :
"The 0.78-A structure of a serine protease: Bacillus lentus
subtilisin.";
                                                                      Match 11.9%; Score 269; DB 1; Length 269; Local Similarity 31.7%; Pred. No. 1e-10; es 98; Conservative 32; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
MEDLINE-92148829; PubMed=1738156;
Betral C., Klupsch S., Papendorf G., Hastrup S., Branner S.
                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Subtilisin Savinase (EC 3.4.21.62) (Alkaline protease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus lentus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1467;
                                         269
26723 MW; 7A03C86D534A1D07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Crystal structure of the alkali
lentus at 1.4-A resolution.";
J. Mol. Biol. 223:427-445(1992).
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MEDLINE-93078250; PubMed=1447775; Sobek H., Hecht H.-J., Aehle W., Schomburg D.; Wecht H.-J., Aehle W., Schomburg D.; Xehruse determination and comparison of two crystal forms of a variant (Ashl15Arg) of the alkaline protease from Bacillus alcalophilus refined at 1.85-A resolution."; J. Mol. Biol. 228:108-117(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000209; Peptidase_S8.
InterPro; IPR000020; Protease_Inhib.
PERM009020; Peptidase_S8; I
PERMO9021; SUBTILISIN.
PROSITE; PR00135; SUBTILASE_ASP; I.
PROSITE; PS00136; SUBTILASE_ASP; I.
PROSITE; PS00137; SUBTILASE_ERP; I.
PROSITE; PS00138; SUBTILASE_ERP; I.
PROSITE; PS00138; SUBTILASE_SER; I.
PROSITE; PS00138; SUBTILASE_SER; I.
PROSITE; PS00138; SUBTILASE_SER; I.
PROFEP 28 112
PROPEP 28 112
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Martin J.R., Mulder F.A., Karimi-Nejad Y., van der Zwan J.,
Martini M., Schipper D., Boellens R.;
Martini M., Schipper D., Eserine protesse PB92 from Bacillus
alcalophilus presents a rigid fold with a flexible substrate-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (VIA CARBONYL OXYGEN)
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EMBL; A13738; CAA01128.1; -.
PIR; A49778, A49778.
PBDB; 1AH2; 15-APR-98.
MEROPS; SO8.038; -.
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MEDLINE=92390330; PubMed=1518788;
van der Laan J.C., Teplyakov A.V., Kelders H., Kalk K.H., Misset O.,
Mulleners L.J.M., Dijkstra B.W.;
"Crystal structure of the high-alkaline serine protease PB92 from
Bacillus alcalophilus.";
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MEDLINE=91282483; PubMed=2059048;
van der Laan J.C., Gerritse G., Mulleners L.J.M., van der Hoek R.A.,
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01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alkaline profease precursor (BC 3.4.21.-).
Bacillus alcalophilus.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
11 TaxID=1445;
                                                                                                                                                                                                                                                                                                         26698 MW; 4D89F8778999BF8D CRC64;
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31.8%; Pred. No. 1e-10;
ive 35; Mismatches 99;
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R EMBL; S48754; AAC60420.1; -.
R EMBL; D11157; BAA02442.1; -.
R EMBL; A225617; CAA01836.1; -.
R EMBL; A22560; CAA01811.1; -.
R EMBL; A22560; CAA01811.1; -.
R EMBL; A22560; GAA01611.1; -.
R EMBL; A22560; GAA01611.1; -.
R ENCOPO; CAA01610.1; -.
R INTERPOS 1 PRO0020; Peptidase S8.
R INTERPOS 2 Peptidase S8; I.
R PROSTIE; PRO0123; SUBTILASE ASP; 1.
R PROSTIE; PS00136; SUBTILASE ASP; 1.
R PROSTIE; PS00136; SUBTILASE ASP; 1.
R PROSTIE; PS00138; SUBTILASE SER; 1.
R PROSTIE; PS00138; SUBTILASE SER; 1.
Hydrolase; Serine protease; Zymogen; Metal-binding; Calcium-binding;
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CALCIUM 1 (BY SIMILARITY).
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CALCIUM 1 (YIA CARBONYL OXYGEN)
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COFACTOR: Binds 2 calcium ions per subunit (By similarity) SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to peptidase family S8.
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CALCIUM 1 (VIA CARBONYL OXYGEN)
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CALCIUM 2 (VIA CARBONYL OXYGEN)
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CALCIUM 2 (VIA CARBONYL OXYGEN)
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TATSLGSTNL - 367
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=21 / ATCC 21522 / JCM 9139 / DSM 2512;
MEDLINE=93043753; PubMed=1368952;
Takami H., Kobayashi T., Kobayashi M., Yamamoto M., Nakamura S.
Takami H., Kobayashi K.;
Aono R., Horikoshi K.;
Aono R., Horikoshi K.;
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 31.8%; Pred. No. 1.6e-10;
Matches 97; Conservative 35; Mismatches 99; Indels 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takami H., Kobayashi T., Kobayashi M., Yamamoto M., Nakamura S. Aono R., Horikoshi K.; "Molecular cloning, nucleotide sequence, and expression of the structural gene for alkaline serine protease from alkaliphilic Bacillus sp. 221."; Biosci. Biotechnol. Biochem. 56:1455-1460(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 42, Last annotation update)
Alkaline protease precursor (EC 3.4.21.-).
Bacilius clausi.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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STRAIN=221 / ATCC 21522 / JCM 9139 / DSM 2512;
HOT:KOShi K.;
(In) Horikoshi K. (eds.);
Microorganisms in alkaline evironments, pp.187-194, VCH, Weinheim (1991).
                                                                                                                                                                                                                                              38853 MW; 539EA72771B6682C CRC64;
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MEDLINE=89326126, PubMed=2546861;

Deane S.M., Fobb F.T., Robb S.M., Woods D.R.;

"Nucleotide sequence of the Vibrio alginolyticus calcium-dependent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARGE RELAY SYSTEM (BY SIMILARITY)
84E96D9C649D4226 CRC64;
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Pred. No. 4.5e-10;
5; Mismatches 152; Indels 128;
                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio.
                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alkaline serine exoprotease A precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detergent-resistant alkaline serine exoprotease A.";
Gene 76:281-288(1989).
-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF041b.; rev;
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE FIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
                                                                                                                                              534 AA
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                                                                                                                                              PRT;
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InterPro, IPR007280; PPC.
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9PIR, J30173, J30173.
HSSP, Q99405; IMPT.
MEROPS, S08.050; -..
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Pfam; PF04151; PPC; 1.
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                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                            Vibrio alginolyticus.
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363
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  GYPSG 302
                                        368 -YGSG 371
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=663;
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P16588;
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MEDITE=92256481; PubMed=1581352;

MEDITE=92256481; PubMed=1581352;

Marinx E., Davall S., Feller G., Gerday C.;

Mucleotide and derived amino acid sequence of the subtilisin from antarctic psychrotroph Bacillus TA39.";

Enochim. Biophys. Acta 1131:111-113(1992).";

Enochim. Biophys. Acta 1131:111-113(1992).";

Enochim. Biophys. Acta 1131:111-113(1992).";

C. I- CATALVITC ACTIVITY: Hydrolysis of proteins and peptide amides.

C. CATALVITC ACTIVITY: Hydrolysis of proteins with broad specificity for peptide bonds, and a preference for a large uncharged residue in P1. Hydrolyzes peptide amides.

C. I- COPACTOR: Blinds 1 calcium ion per subunit (Potential).

C. I- SUBCELLULAR LOCATION: Secreted.

C. MISCELLANEOUS: Still active at temperatures close to 0 degrees constituted in has a marked heat lability.

C. MISCELLANEOUS: Secretion of subtilisin is associated with onset of sporulation, and many mutations which block sporulation at early stages affect expression levels of subtilisin. However, subtilisin is not necessary for normal sporulation.

C. SIMILARITY: Belongs to peptidase family S8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 VNEATALATGGKATYSFQAQAGKPLKISLVWTDAPGSTTASYTLVNDLDLVITAPNGQKY 379
                                                                         344
                                                                                                                                                      283
                                                                                                                                                                                              ---TDVGLGYPSG-----DQGWGRVTLDKSLNVAY 319
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PNSGTISAPGTAKNAITVGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPG 223
                                                                                                                                                                                                                                                                                                                                                             303 ADACNYS-PARVATGVTVGST-----TSTDARSSFSNWGSC-----VDVFAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GLSGSSGQVAYYYVDVEAGQRLTVQM-------YGGSGDADLYLRF--GAK-
                                                                                                                                                  TFILSARSSLAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKFSL
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Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Subtilisin precursor (EC 3.4.21.62).
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Pfam; PF00082; Peptidase_S8: 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00116; SUBTILASE_ASP; 1
PROSITE; PS001137; SUBTILASE_HIS; 1
                                                                                                                                                                                                                                                                                                    284 IKAALIAGA------
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PIR; S23407; S23407.
HSSP; Q99405; IMPT.
MEROPS; S08.UPA; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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31.5%; Pred. No. 4.5e-10;
ive 34; Mismatches 101; Indels
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Best Local Similarity 31.5%
Matches 96; Conservative
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                 SOLUTION TO THE TERMINE TO THE TRANSPORT OF THE TRANSPORT
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X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).

X Goddette D. W., Paech C., Yang S.S., Mielenz J.R., Bystroff C.,

A Goddette D. W., Paech C., Yang S.S., Mielenz J.R., Bystroff C.,

Wilke M.E., Fletterick R.J.;

"The crystal structure of the Bacillus lentus alkaline protease,

WILK M.E., Fletterick R.J.;

"The crystal structure of the Bacillus lentus alkaline protease,

"The crystal structure of the Bacillus lentus alkaline protease,

"The crystal structure of the Bacillus.";

"Mol. Biol. 128:580-585(1992).

"I catalyzes the hydrolysis of proteins and peptide amides.

"I catalyzes the hydrolysis of proteins with broad specificity

for peptide bonds, and an preference for a large uncharged residue

"In Pl. Hydrolyzes peptide amides."

"I copactors Binds 2 calcium lons per subunit."

"I subschilding Secretion of Subtilisin is associated with onset of sporulation, and many mutations which block sporulation at early

"I since the esseary for normal sporulation."

"I similarity: Belongs to peptidase family S8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 SWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATENY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 WANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGY 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 ALADGGTGNGV-YGVAPDADLMAYKVLGDDGSGYADDIAAAIRHAGDQATALNTKVVINM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 SLGSSGESSLITNA---VNYSYNKGVLIIAAAGNSGPYQGSIGYPGALVNAVAALEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GQGQVVAVADTGLDTGRNDSSMHEAFRGKITAL--YALGRT----NNANDFNGHGTHVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 GGGINIAVLDÍGVNÍN-----HPDLRNNVEQCKDFTVGTÍYINNSCTDRQGHGÍHVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPSFGSLADNPNHIAQFSSRG-----ATRDGRIKPDVTAPGTFILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59; Gaps
       PROSITE; PS00138; SUBTILASE SER; 1.
Hydrolase; Spornlation; Serine protease; Zymogen; Metal-binding; Signal.
SIGNAL.
SIGNAL.
PROPER 27 11 POTENTIAL.
CHAIN
ACT_SITE 145 145 CHARGE RELAY SYSTEM (BY SIMILARITY)
ACT_SITE 182 182 CHARGE RELAY SYSTEM (BY SIMILARITY)
ACT_SITE 180 CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                         11.7%; Score 263.5; DB 1; Length 29.0%; Pred. No. 4.1e-10; ive 46; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2003 (Rel. 42, Last sequence update)
Subtilisin BL (EC 3.4.21.62) (Alkaline protease).
Bacillus lentus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                           CALCIUM (POTENTIAL).
CALCIUM (POTENTIAL)
AE4F121BD32B26EC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                          44086 MW;
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                                                                                                                                                                                                                                                                                                                                          154
420 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 92; Conserv
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SUBB_BACLE
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14; 72 99

Gaps

74;

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                                   AGTIAALNNSIGVLGVAPSAELYAVKVLGADG--RGAISSIAQGLEWAGNNGMHVANLSL 124
                                                                                                                                                               175 -----bonnnrasrsoygagi-----bivapgvnvostyp------gstyas 210
                                                                                                                                                                                                                  AGSV -- LCNALN-KGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNAGARIHTNSW 129
                                                                         GAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATENYRP 189
                                                                                                      GSP---SPSATLEQAVNSATSRGVLVVAASGNSGASS--ISYPARYANAMAVGAT---- 174
                                                                                                                                                                                                250 MGGTSMATPIVAGNVA------QLREHFIKNRGITPKPSLIKAALIAGATDVGL 297
                                                                                                                                   SFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFWANYNSKYAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20067863; PubMed=10588904;
Smith C.A., Toogood H.S., Baker H.M., Daniel R.M., Baker E.N.;
Smith C.A., Toogood H.S., Baker H.M., Daniel R.M., Baker E.N.;
Calcium-mediated thermostability in the subtilisin superfamily: the crystal structure of Bacillus Ak.1 protease at 1.8-A resolution.";
J. Mol. Biol. 294:1027-1040(1999).
-!- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MISCELLANEOUS: Has a pH optimum of 8.5, a temperature optimum of 75 degrees Celsius.
-!- SIMILARITY: Belongs to peptidase family SB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-95083562; PubMed-7993087;
Maciver B., McHale R.H., Sull D.J., Bergquist P.L.;
"Cloning and sequencing of a serine proteinase gene from a thermophilic Bacillus species and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Thermophilic serine proteinase precursor (EC 3.4.21.-) (Ak.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease).
Bacillus sp. (strain AKI).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli.";
Appl. Environ. Microbiol. 60:3981-3988(1994).
[2]
                                                                                                                                                                                                                                                                                                                                                                   401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro, IPR000209, Peptidase S8.
Interpro, IPR009020, Protease Inhib-
Pfan, PR0082, Peptidase S8, I
PRINTS; PR00723, SUBTILISIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00723; SUBTILLISIN, PROSITE; PS00136; SUBTILLASE ASP; 1. PROSITE; PS00137; SUBTILASE HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L29506; AAA63688.1; -. PIR; 139974; 139974. PDB; 1DBI; 18-NOV-99.
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                                                                                                                                                                                                                                                                                        257 -YGSG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S08.009; -
                                                                                                                                                                                                                                                          298 GYPSG 302
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Q45670;
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137 QNTYTDYAWDVTKGSSGQEIAVIDTGVD-----YTHPDLDGKVIKGYDF--VDNDYDPM 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P54423, 006726, 01.00 Created) 15-DEC-1996 (Rel. 34, Created) 15-DEC-1998 (Rel. 34, Last sequence update) 10-OCT-2003 (Rel. 37, Last annotation update) 10-OCT-2003 (Rel. 42, Last annotation update) 20-CELL wall-associated protease precursor (EC 3.4.21.-) [Contains: Cell wall-associated polypeptides CWBP23 and CWBP52]. Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 SGAEVINLSLGC---DCHTTLENAVNYAWNKGSVVVAAAGNNG--SSTTFEPASYENVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 AVGAVDQY-----DRLASFSNYGTW-----VDVVAPGVDIVSTIT-----
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MEDLINE=97158234; PubMed=9004506;
Margot P., Karamata D.;
The wpra gene of Bacillus subtilis 168, expressed during exponential growth, encodes a cell-wall-associated protease.";
Microbiology 142:3437-3444(1996).
                                                                                                                                                QNNYGLY------GQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDP-
                                                                                                                                                                                                                                                                                                --NGHGTHVAGSVLGNALN----KGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWN
                                                                                                                                                                                                                                                                                                                                                                            189 DLNNHGTHVAGIAAAETNNATGIAGMAPNTRILAVRALDRNG--SGTLSDIADAIIYAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 AGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSF
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MEDLINE=98015415; PubMed=9353931;
Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.;
"Sequencing of regions downstream of addA (98 degrees) and citG (289 degrees) in Bacillus subtilis.";
Microbiology 143:3305-3308(1997).
                                                                            58;
        Length 401;
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                        66
Query Match
Best Local Similarity 31.7%; Pred. No. 1.4e-09; Matches 85; Conservative 26; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 WANYNSKYAYMGGISMATPIVAGNVAQL 267
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MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Mosetl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Rarro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
A Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha B., Roche M., Sadaie Y.,
A Schiguchi J., Schoska A., Schoeter R., Socffone F.,
Schileich S., Schroeter R., Socffone F.,
A Scrotin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
A Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vasarotti A.,
A Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasarotti A.,
Minters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
A Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
Rubtilis.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 VVAVADIGLDIGRNDSSMHEAFRGKITALYA---LGRINNANDPNGHGTHVAGSVLGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 N----KGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNAGARIHTNSWGAPVNGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511 NGYSMTGLNAKAKIIPVKVLDSAG--SGDTEQIALGIKYAADKGAKVINLSLG----GGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANSROVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATENYRPSFGSLADN
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SIMILARITY).
SIMILARITY).
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POTENTAL.
CWBP52.
CWBP52.
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I - A (IN REF. 1).
W, OF67C353ES5F8DBC CRC64;
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Subtilist; BG11846; wprA.
InterPro; IPR00209; Peptidase_S8.
Pfam, PF00082; Peptidase_S8.1.
PROSTE; PR00723; SUBTILISIN.
PROSTE; PS00136; SUBTILASE_ASP; FALSE_NEG.
PROSTE; PS00138; SUBTILASE_ESR; 1.
PROSTE; PS00138; SUBTILASE_ESR; 1.
Hydrolase; Serine protease; Cell wall; Zymogen; Signal;
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J. Biol. Chem. 265:3167(1990).
J. Biol. Chem. 265:3167(1990).
J. FUNCTION: THIS VIRULENCE FACTOR OF S.PYOGENES SPECIFICALLY CLEAVES.
THE HUMAN SERUM CHEMOTRAKIN CSA AT LYS(68)-ASP(69) BOND NEAR ITS.
C.TERMINUS, DESTROYING ITS ABILITY TO SERVE AS A CHEMOATRACTANT.
J. SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).
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MEDLINE=90153964; PubMed=2406246;
Chen C.C., Cleary P.P.;
"Complete nucleotide sequence of the streptococcal C5a peptidase gene
                                                                                                                                                                                                                                  PYAAAAAGLL---FAQNPKL--KRTEVEDMLKKTADDISFESVDGGEEELYDDYGDPIEI
                           PNHIAOFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFWANYNSKYAYMGGTSMAT
                                                                                               MDMTADFSNYGKGL-----DISAPGSDI----PSLVP-----NGNVTYMSGTSMAT
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Pfam; PF02225; PA; I anchor; 1.
Pfam; PF00225; PA; I anchor; 1.
PF03175; PR00723; SUBTILASE SB; 1.
PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00136; SUBTILASE HS; 1.
PROSITE; PS00137; SUBTILASE HS; 1.
PROSITE; PS00138; SUBTILASE ERR; 1.
Hydrolase; Serine protease; Cell wall; Peptidoglycan-anchor; Repeat;
                                                                                                                                                                          PIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYPSGDQ----
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01-APR-1990 (Rel. 14, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
CSA peptidase precursor (EC 3.4.21.-) (SCP).
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InterPro; IPR003137; PA.
InterPro; IPR001009; Peptidase_S8.
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PIR; A35066; A35066.
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291 TSAGNDSSFGGKTRLPLADHPDYGVVGTPAAADSTLTVASYSPDKQLTETAMVKTDDQQD 350
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CSA PEPTIDASE.
REMOVED BY SORTASE (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
4 X 17 AA THADHMENT DOMAIN (POTENTIAL)
4 X 17 AA TANDEM REPEATS.
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AMIDE-LINKED TO CELL WALL (F
MW; DZDDC52E5752DA5D CRC64;
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; Pred. No. 2.6e-08;
65; Mismatches 164;
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March 31, 2004, 15:58:03 ; Search time 32.475 Seconds (without alignments) 4206.909 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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1: Sp_archea:*
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5: Sp_numan:*
5: Sp_numan:*
6: Sp_numan
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Score Match Length DB ID Description

1 2261 100.0 433 2 Q9AQR1 Q9aqr1 bacillus sp Q9aqr2 bacillus sp Q9aqr2 bacillus sp Q9aqr2 bacillus sp Q9aqr3 2 Q9AQR4 Q9aqr2 bacillus sp Q9aqr2 bacillus sp Q9aqr3 2 Q9AQR2 Q9aqr3 bacillus sp Q9aqr3 B8.6 639 2 Q9AQR3 Q9aqr3 bacillus sp Q9aqr3 B8.6 640 2 Q93UV9 Q9aqr3 bacillus sp Q9aqr3 Bacillus pa Q9aqr3 Bacil

Q8rc68 thermoanaer	Q8kkh6 streptomyce		Q910a0 streptomyce	Q82i39 streptomyce	Q45464 bacillus sp	093635 thermococcu	Q9r154 streptomyce		_	O31788 bacillus su	Q9p9ll pyrococcus	Q9kem1 bacillus ha	Q9p9d1 uncultured	4	Q54437 staphylothe	Q82cf0 streptomyce	Q8pms7 xanthomonas	Q98316 bacillus sp	æ	P70765 alteromonas	Q8pnw1 xanthomonas	054327 bacillus sp	Q8gcw3 streptococc	Q8gb52 vibrio sp.	Q8pal8 xanthomonas	Q8pb28 xanthomonas	Q93iq4 xanthomonas	Q8e2v6 streptococc
S QBRC68	Q8KKH6	Q8GGT4	6 Q9L0A0	6 Q82I39	Q45464	093635		6 Q82BI4			Q9P9L1	6 Q9KEM1	Q9P9D1	6 Q816G4	Q54437		6 Q8PMS7	915S6Q	5 Q9L1Z8	P70765	S Q8PNW1	054327	Q8GCW3	Q8GB52		6 Q8PB28	Q931Q4	6 Q8E2V6
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343.5	343	341.5	338	N	a	328	~	327	324	315.5	309	302.5	290.5	289.5	285	284.5	281.5	279	277.5	272.5	271	269	266.5	266	266	265	264	260.5
17	18	19	20	21	22	23	24	25	. 26	27	28	29	30	31	32	33	34	3	36	37	38	9	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1
09AQR1 DO COAGR1

DO COAGR1

AC COAGR1

COAGR1

TO COAGR1

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Hydrolase, Protease, Serine protease.
NON TER 1 1
NON TER 433 433
SEQUENCE 433 AA, 45636 MW, 52087E
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
Protease (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
A Horikoshi K.;

I alkaliphilic Badilus subtilisin-like serine proteases from
alkaliphilic Badilus sep: enzymatic properties, sequences, and
revolutionary relationships.";

Biochem. Biophys. Res. Commun. 279:313-319(2000).

I SimilaRITY: Belongs TO PEPTIDASE FAMILY SS.

REMBI, ABO44402; BAB11265.1;
ROSP, OG:0004289; F:subtilase activity; IEA.
GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:0004289; F:subtilase activity; IEA.
ROSP GO:000508; P:proteolysis and peptidolysis; IEA.
RICEPPRO; IPR007280; Peptidase_SS.
R Ffam; PF00082; Peptidase_SS.
R Pfam; PF001815; PeC; 1.
R Pfam; PF001815; PeC; 1.
                                      Gaps
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             Length 433;
                                     Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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Last annotation update)
           100.0%; Score 2261; DB 2;
100.0%; Pred. No. 1.8e-124;
ive 0; Mismatches 0;
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MEDLINE=20568675; PubMed=11118284;
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PROSITE; PS00137; SUBTILASE HIS;
PROSITE; PS00138; SUBTILASE SER;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
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                                      Matches 433; Conservative
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             Query Match
Best Local Similarity
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A Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
A Horikoshi K.; Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
A Horikoshi K.; Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
A Horikoshi K.; Okuda M., Hatada M., Saelin Britanin Biophys Res. Commun. 279:313-319(2000).
C Biochem. Biophys Res. Commun. 279:313-319(2000).
C SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
R HSSP; Q45670; IDBI.
R HSSP; Q45670; IDBI.
R GO: GO:0004289; F:subtidase activity; IEA.
GO: GO:0004289; F:subtidase activity; IEA.
GO: GO:000508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR00220; Peptidase_S8.
R InterPro; PR00220; Peptidase_S8: 1.
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                                                                                 Length 433;
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Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=133779;
433
45636 MW; 52087E0A2516107F CRC64;
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Last sequence update)
Last annotation update)
                                                                           99.6%; Score 2251; DB 2;
llarity 99.3%; Pred. No. 7.1e-124;
Conservative 1; Mismatches 2;
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STRAIN=9860,
MEDLINE-20568675; PubMed=11118284;
Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
Borikoshi K.,
"Novel oxidatively stable subtilisin-like serine proteases from
alkaliphilic Bacillus ssp.: enzymatic properties, sequences, and
evolutionary relationships";
Biochem. Biophys. Res. Commun. 279:313-319(2000).
                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                    DB 2; Length 434;
                                                                                                                                                                                                                                                                Query Match

89.5%; Score 2024.5; DB 2; Length
Best Local Similarity 88.5%; Pred. No. 1.3e-110;
Matches 384; Conservative 28; Mismatches 21; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR007289; PPC
Pfam; PPC0412; Peptidase_S8; 1.
Pfam; PF04121; PPC; 1.
PRINTS; PR00127; SUBTILISIN.
PROSITE; PS00137; SUBTILIASE_HIS; 1.
PROSITE; PS00138; SUBTILIASE_SER; 1.
PHYDROLAGE; Protease; Serine protease.
NON TER 434 434
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Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
Horikoshi K.;
"Novel oxidatively stable subtilisin-like serine proteases from
alkaliphille Bacillus ssp.: enzymatic properties, sequences, and
evolutionary relationships.";
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=133781;
                                                                                                                                                 45587 MW; B81291A803C775AE CRC64;
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Last annotation update)
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-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SB.
EMBL, AB046406; BAB21269.1; -..
HSSP, 90:00782; ISP.
GO; 90:000823; F:peptidase activity; IEA.
GO; GO:0004289; F:subtilase activity; IEA.
                                                                                                                                                                                   Query Match
99.1%; Score 2240; DB 2;
Best Local Similarity 98.8%; Pred. No. 3.1e-123;
Matches 428; Conservative 4; Mismatches 1;
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                     PRINTS, PRO0723; SUBTILISIN.
PROSITE; PS00137; SUBTILIASE HIS; 1.
PROSITE; PS00139; SUBTILIASE SER; 1.
Hydrolase; Procease; Serine procease.
NOW TER. 433 433
SEQUENCE 433 AA; 45587 MW; B81291
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01-JJM-2001 (TrEMBLrel, 17,
01-JJM-2001 (TrEMBLrel, 17,
01-JJM-2003 (TrEMBLrel, 24,
Protease (Fragment).
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        Pfam; PF04151; PPC; 1
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                                                                                                                                                Gaps
                                                                                                                                               1;
                                                                                                                        Query Match 88.6%; Score 2002.5; DB 2; Length 639; Best Local Similarity 88.2%; Pred. No. 4.1e-109; Matches 383; Conservative 26; Mismatches 24; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN.KF4.;

Itoh S., Saeki K.;

"new procease.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

GO:0000439; F:subtilase activity; IEA.

GO:00006508; F:subtilase activity; IEA.

InterPro: IPR000209; Peptidase_S8.

InterPro: IPR007280; PPC.

InterPro: IPR007280; PPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus sp. KSM-KP43.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=109322;
                                                                                                     316AF6FFDBE4FF54 CRC64;
    MOST, COUGESS, TSUDDIJABE ACTIVITY, IEA.

GO; GO:0006208; P:subbilabe activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR000209; Peptidase_SS.

Pfam; PF00082; Peptidase_SS; 1.

Pfam; PF00151; PPC; 1.

PRINTS; PR00173; SUBTILIASE HIS; 1.

PROSITE; PS00139; SUBTILIASE HIS; 1.
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01-OCT-2002 (TrEMBLrel. 22,
01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                           Query Match

88.4%; Score 1998.5; DB 2; Length 640;
Best Local Similarity 87.6%; Pred. No. 7e-109;
Matches 381; Conservative 28; Mismatches 24; Indels 1;
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PRINTS; PR00722; SUBTILISIN.
PROSITE; PS00134; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
SEQUENCE 640 AA; 67991 NW; 4BBAF77E9D592C15 CRC64;
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
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Best_Local Similarity 26.1% Matches 142, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSSLA-----PDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREH------FIK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRGITPKPSLIKAALIAGATDVGLGYPSGD--------QGWGRVTLDKS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIKLQPIGSLIKALMINNAQLINGTFPLSSTNTNPSNAVFDTFAGANFVQGWGSLRMSEW 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 LNVAYVNEA------QAQA 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 GTHVCGSAAGAPEDSSLAISSFSGLAIDAKIAFFDLASDPSNNEPVPPEDYSQLYQPLYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L---YVESSGVKPKPSRWVGIGELGKDKKASNWKEYSLSTGQNVSYCFTYKPSSSGSNSG
                                                                                                                                                                                                                                                                                                                                                                                                    19 LYGOGOVVAVADIGLDIGR---NDS----SMHEAFRGKIIALYALGRINNANDPNGH
                                                                                                                                                                                                                                                                                                                                                                                                                                 GTHVAGSVLGN-----ALN--KGMAPQANLVFQSI-MDSSGGLGGLPSNLNTLFSQAWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGARIHTNSWGA----PVNGAYTANSRQVDEYVRNN-DMTVLFAAGNEGPNSGTISAPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKNAITVGATE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKNVITVGAEQTTHESYTTDALEYSNFETVAKSTLNSLCQSFDDKYCTYTTAQCCTEYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------NYRPSFGSLAD--NPNHIAQFSSRGATRDGRIKPDVTAPGTFILSA
                                                                                                                                                                                                                                                                                                             20.6%; Score 465; DB 5; Length 1825; 26.9%; Pred. No. 1.4e-18; ive 79; Mismatches 167; Indels 17
R InterPro; IPR003439; ABC_transporter.

InterPro; IPR00209; Peptidase_S8.

Pfam; PF00064; ABC_tran; 1.

R Pfam; PF00005; ABC_tran; 1.

R PRINTS; PR00723; SUFILISIN.

R PRINTS; PR00723; SUFILISIN.

R PRODOM; P0000006; ABC_transporter; 1.

R PROSITE; SN00382; AAA; 1.

R PROSITE; PS00211; ABC_TRANSPORTER_1; 1.

R PROSITE; PS00137; SUBȚILASE_HIS; 1.

R ATP-binding; Protease; Transport.

SEQUENCE 1825 AA; 202641 MW; E28160BC78613A3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDSINNVEGIIYTPINTKSEISFRFIIAGTNIPIGPQNFS 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WDGRNNVENVF---INAPQSGTYTIEVQAYNVPSGPORFS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBL_TaxID=44689;
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Last sequence update)
Last annotation update)
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(TrEMBLrel. 16, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 26.9
Matches 156; Conservative
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01-MAR-2001 (
01-MAR-2001 (
01-OCT-2003 (
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Q9GTN7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 -GITPKPSLIKAALIAGAT---DVGLGYPSGDQGWGRVTLDK------SLNV-AYV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEATALA-TGOKATYSFQAQAGKPLKISLVWTDAPGSTTASYTLVNDLDLVITAPNGQKY 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGNDFSYPYDNN-------WDGRNNVENVFINAPQSGTYTIEVQAYNVPSGPORF 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWGAPVNGAYTANSRQVDEYVRNN-DMTVLFAAGNE---GPNS-GTISAPGTAKNAITVG 182
                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 APDSSFWANY-----NSKYAYMGGTSMATPIVAGNVAQLRE-----HFIKNR----
                                                                                                                                                                                                                                                                                                                                                                                                                 18 GLYGQGQVVAVADTGLDTGR---NDSSMHEAFRGKITALYALGRTNNANDPNGHGTHVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 SVLGNAL-----NKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNAGARIHTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P----NHIAQ-----NHIAQ------FSSRGATRDGRIKPDVTAPGTFILSARSSL
                                                                                                                                                                                                                                                                                                                                                                                           143;
                                                                                                                                                                                                                                                                                                                                                                   Length 1702;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 ATENYRPSFGSLAD------
                                                                                                                                                                                                                                                                                                    PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
ATP-binding; Transport
SEQUENCE 1702 AA; 187103 MW; 4A67716303CB7131
                                                                                                                                                                                                                                                                                                                                                                 19.5%; Score 441.5; DB 5; 26.1%; Pred. No. 3e-17; tive 91; Mismatches 168;
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561 AA

PRELIMINARY;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 THVAGSVLG----NALNKGMAPQANLVFQSIM--DSSGGLGGLPSNLNTLFSQAWNAGA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 RIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 YNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITP---KPSLIKAALIAGATDVG-LG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 INDYYTAAPGTSMATPHVAGIAALLLQ---AHPSWTPDKVKTALIETADIVKPDEIADIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 NYGLYGOGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNAN-----DPNGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 YPSGDOGWGRVTLDKSLNVAYVNEATALATGOKA----TYSFOAQAGKPLKISLVWTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGSTTASYTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYTI
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                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=Vol./ DSM 3638 / ATCC 43587 / JCM 8422;

Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

"The complete sequence of the Pyrococcus furiosus genome.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

R GG; GG:0008233; F:peptidase activity; IEA.

R GG; GG:0008233; F:peptidase activity; IEA.

R GG; GG:0008239; F:subtilase activity; IEA.

R GG; GG:0008239; F:subtilase activity; IEA.

R FAG; GG:000823; F:gubtilase activity; IEA.

R PROSITE; PSO0136; SUBTILASE ASP; I.

R PROSITE; PSO0136; SUBTILASE ASP; I.

R PROSITE; PSO0138; SUBTILASE HS; I.

R PROSITE; PSO0138; SUBTILASE ERR; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17; Length 654;
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                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                        Created)
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                                                                                   Q8U0C9 PRELIMINARY;
Q8U0C9;
01-JUN-2002 (TrEMBLrel. 21, C.
01-JUN-2002 (TrEMBLrel. 24, L.
01-JUN-2003 (TrEMBLrel. 24, L.
Alkaline serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVVSY---SGSANYQVDVV
                                                                                                                                                                                                                                                       Pyrococcus furiosus
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368 TAAK-----ANSVNGYVTYSGTSMATPFVAGTVALMIN---ANPNITPNDA--KN 412 ::: | :: | :: | | : | | | : :: | | :: | | :: | | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | 226 315 YTIGSPGAAEKAITVAAMAD----VGELGFN---LASFSSKGPTADGRIKPDIAAPGYNI 367 LSARSSLAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKA 286 287 ALIAGAIDVGLGYPSGDQGWGRVTLDKSLNVA------YVNEATALATGQKAT 333 334 YSFQA-QAGKPLKISLVWTDAPGSTTASYTLVNDLDLVITAPNGGKYVGNDFSYPYDNNW 392 107 PSNLNTLFSQAWNAGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNS 166 262 VQNKDVYGIKVINLSLGTSTSSDG--TDSTSLAVNFAVD-----SGIVVVVAAGNSGPAK 314 SEQUENCE FROM N.A.

STRAIN=MB4 / JCM 11007;

MEDLINE=21992816; PubMed=11997336;

A MEDLINE=21992816; PubMed=11997336;

A MEDLINE=21992816; PubMed=11997336;

A Chen Y., Xue Y., Xu Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

A Chen Y., Xue Y., Xu Y., Li W., Yang H.;

A Complete sequence of T. tengcongensis genome.";

B Complete sequence of T. tengcongensis genome.";

Complete sequence of T. tengcongensis genome.";

B Complete sequence of T. tengcongensis genome.";

Complete sequence of T. tengcongensis guartiase Asp;

InterPro; IPR002048; EF-hand.

DR PROSITE; PR00723; SUBTILASE ASP;

DR PROSITE; PR00134; SUBTILASE ASP;

PROSITE; PR00134; SUBTILASE SER; 1.

PROSITE; PR00134; SUBTILASE SER; 1. 64 ----DPNGHGTHV----AGSVLGNALNKGMAPQANLVFQSIMDSSG-----GLGGL 202 TTPYDDNGHGTHVASIAAGTGAGNSFYKGVAPDALLVGIKVLDANGSGSMSTVTAGIDWA 6 GIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNAN---167 GTISAPGTAKNAITVGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFI Gaps 93; DB 16; Length 561; Q8RBJ2; QBTBJ2; QBTBJ2; Q1-UTN-2002 (TEMBLEE]. 21, Created) O1-OCT-2003 (TEMBLEE]. 25, Last sequence update) O1-OCT-2003 (TEMBLEE]. 25, Last annotation update) Subtlishin-like serine proteases. APRE2 OR TTEOSE. Thermoanaerobacter tengcongensis. Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacteriales; MCBI_TaxID=119072; Query Match
17.8%; Score 402.5; DB 16; Length
Best Local Similarity 31.0%; Pred. No. 1.3e-15;
Matches 142; Conservative 63; Mismatches 160; Indels 59968 MW; BA9C5C52F7083A18 CRC64; DGRNNVENVFINAPQSGTYTIEVQAYNVPSGPQRFSLA 430 Protease, Complete proteome SEQUENCE 561 AA; 59968 M 227 393 g

288

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545 VILELSVAATHAPEGVFRLSASRVTVPAHGTADVTLTIDGSGSAGGRAYSGQILA---T 600
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                                                                     RTNNANDPNGHGTHVAGSVLGNAL----NKGMAPQANLVFQSIMDSSGGLGGLPSNLNT 112
                                                                                                                                                                                                          113 LFSQAWNAGARIHTNSWGA-PVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGFNSGTISA 171
                                                                                                                                                                                                                                                                            332 MEWAAVERHAKIVNMSLGSGEQSDGSDPMSRAVDRLSAQTGALFVVAAGN-GGEAGSIGA 390
                                                                                                                                                                                                                                                                                                                                                                                          ----NSSFAAGGNGAYQSLSGTSMATPHVAGAAALL-----AAARPDLSGSALKDV 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 IAGATDVGLGYPSGDQGWGRVTLDKSLNVAYVNEATALATGQK-----ATYSFQAQAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 KPLKISLVWTDAPGST---TASYTLV---NDLDLVIT-----APNGQKYVGNDFSYPYDN 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNANDPNGHGTHVAGSVLGN-ALN----KGMAPQANLVFQSIMDSSGGLGGLPS----- 108
                                                                                                              273 PDENTDDRDGHGTHVASTIAGTGAASAGKEKGVAPGARLSIGKVLDNS-GRGQISWTLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 LASSSHRIPRYDAFQAGSGRVDVDAAVRAGVYASAIAYAPGSSPGPVRRLVTYINTIGAA
                                                                                                                                                                                                                                                                                                                                              PGTAKNAITVGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 SLAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAAL---
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Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 34.5%; Pred. No. 2.7e-14;
Matches 119; Conservative 48; Mismatches 119; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBI_TaxID=182710;
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BMBL; AP004601; BAC14331.1; -
GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro. IPR00020; Peptidase S8; I.
PRANTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILIASE ASP; I.
PROSITE; PS00137; SUBTILIASE ASP; I.
PROSITE; PS00137; SUBTILIASE ASP; I.
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SEQUENCE 430 AA; 45838 MW; 6D09A99BBC1E310F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 NWDGRNNVENVFINAPQSGTYTIEVQAYNVPSGPQRFSLAI 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBENVI;
01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Intracellular alkaline serine proteinase.
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STRAIN=HTE831 / DSM 14371 / JCM 11309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21996410; PubMed=12000953; Bentley S.D., Charles K.F., Cerdeno-Tarraga A.-M., Challis G.L., Bentley S.D., Charer K.F., Cerdeno-Tarraga A.-M., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Seeger K., Saunders D., Sharp S., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL: AL999130; CACO1588.1; -.
HSSP; Q99405; 1MPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.5%; Score 395.5; DB 16; Length 1239; 30.6%; Pred. No. 9.6e-15; ive 55; Mismatches 172; Indels 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STAIN=A3.(2);
Cerdeno, A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR003137; PA.
InterPro; IPR003197; PA.
   516 TGTQRQETITILPSQTGTYYVKVYSYR-GSGNYFFDLS 552
                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Putative secreted peptidase.
SCO7188 OR SC8A11 16C.
                                                                                                                                                                            PRT; 1239 AA
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Pfam; PF00082; Peptidaee S8; 1.
PRINTS; PROO723; SUBTILLSIN.
PROSITE; PS00136; SUBTILLASE ASP; 1.
PROSITE; PS00137; SUBTILLASE HIS; 1.
PROSITE; PS00138; SUBTILLASE SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
MEDLINE=97000351; Pubmed=8843436;
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Best Local Similarity 30.6
Matches 141; Conservative
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                                                                                                                                                                         PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
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SEQUENCE 1239 AA
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Saunders D.C.
                                                                                               RESULT 11
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Matches
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                                                                                                     173 EPYDD-NGHGTHCAGDDAAGNGALSDGQYQGPAPDANLVGVKVLNKTGS-GSLSTVIEGID 230
                                                                                                                                      220 TAPGTFILSARS--SLAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGI 277
                                                                                                                                                       231 WCIQNQSKYNINIL---SL&LGSDATEPAEGDPVVNAV------ETAWDNGMVVCVAA
                                      -----NINTLFSQAMNAGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAA
                                                                                       160 GNEGPNSGTISAPGTAKNAITVGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2) / W145;

MEDLINE=21996410; PubMed=12000953;

MEDLINE=21996410; PubMed=12000953;

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chan C.W., Collins M.,

Harper D., Bateman A., Brown B., Chandra G., Chan C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitesch E., Rajandream M.A., Rutherford K., Rutter S.,

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinsahi H., Hopwood D.A., As to Confect cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                      T--PNQVKEKLMEACQD--LGQSPNVQGAGYL---NAANLININE 430
                                                                                                                                                                                      TPKPSLIKAALIAGATDVGLGYPSGDQGWGRVTLDKSLNVAYVNE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      _3 D.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0008233; F:peptidase activity, IEA.
GO:0004289; F:subtilase activity; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97000351; PubMed=8843436;
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EMBL; AL939130; CAC01576.1; -.
HSSP; Q99405; IMPT.
                                                                                                                                                                                                                                                                                                                                         Putative secreted peptidase. SC07176 OR SC8A11.04C.
                                                                                                                                                                                                                                                                             PRELIMINARY;
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Submitted (AUG-2000) t
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 OSLSGTSMATPHVAGAAALLAAEH------PDWTGQRLKEALV-GTTAGTQRFSPF 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOGWCRVTLDKSLNVAYVNEATALATG-------QKATYSFQAQAGKPLK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 ISLVWTDA-----LVITAPNGQK 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612 LART----PVGVNKEGRR--ATLALTAKDHHDKPLSGTVILKDVERN--TAPKVYSV 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 GIGAASGGVEKGVAPGASLHIGKVLDNSG--SGQDSWV--LAGMEWAVRDQHAKIVSMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNTGEGVGVAVLDTGVDAG-----HPDFAGRIAATASFVPDQDVTDRNGHGTHVASTVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G----NALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAW---NAGARIHTNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 GDSPTDGT-DPLSEAVNWLSAETGALFVVAAGNSGPEAYTVGTPAAADAALTVGAVNGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 PSFGSLADNPNHIAQFSSRG-ATRDGRIKPDVTAPGTFILSARSSLAPDSSFWANYNSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 KGVDQLAD-----FSSRGPRVGDNAVKPDLTAPGVGVLAARSRYAPEG-----EGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 AYMGGISMATPIVAGNVAQL-REHFIKNRGITPKP----SLIKAALIAGATDVGLGYPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYGOGOVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNGHGTHVAGSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 YVGNDFSYPYDNNWDGRNNVENVFINA-----POSGTYTIEVOAYNVPSGPORFSL
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from
                                                                                                                                                                                                                                                                                                                                 15.8%; Score 357; DB 16; Length 1253;
.larity 30.0%; Pred. No. 1.7e-12;
Conservative 53; Mismatches 165; Indels 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Subtilisin-like protease.
Streptomyces albogriseolus.
Bacteria; Actinobacteria; Actinomycetales;
                                                                                                                                                                                                                                                                          1253 AA; 130971 MW; AA69B417EFEEDB89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJINE-97144528; PubMed=8990295; Suzuki M., Taguchi S., Yamada S., Kojima S., Miura K., "A novel member of the subtilisin-like protease family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         StreptomyCes albogriseolus.",
J. Bacteriol. 179:430-438(1997).
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GO; GO:0008233; F:peptidase activity; IEA
                                InterPro) IPR000209; Peptidase_S8.
Fiam, PR02225; PA; 1.
Pfam, PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
Complete proceome.
SEQUENCE 1253 AA; 130971 MW; AA
InterPro; IPR003137; PA.
InterPro; IPR000209; Peptidase_S8
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HSSP; P00782; 2SBT.
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                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 143; Conserv
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completed: March 31, 2004, 16:09:00
Ne : 34.475 secs
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es 116; Conserv
                                                                                                                                                                                                        Hydrolase;
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                                                                                                                                                                                                                    SÉQUENCE
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Matches
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                                                                                                                                                                                                                                                                  212 GYDGKGVKIAVLDTGVD-----ATHPDLKGQVTASKNFTSAPTTGDVVGHGTHVASIAA 265
                                                                                                                                                                                                                                                                                                                                                                                    322 GMDTPETDPLEAA------VDKLSAEKGILFAIAAGNEGPQS--IGSPGSADSALIVGA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 YNSKYAYMGGISMAIPIVAGNVAQLREHFIKNRGITP--KPSLIKAALIAGAIDVGLGYP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNALN-----KGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA--GARIHTNSWG 130
                                                                                                                                                                                                                                                                                                                          266 GTGAQSKGTYKGVAPGAKILNGKVLDDA----GFGDDSGILAGMEMAAAQGADIVNMSLG 321
                                                                                                                                                                                                                                                                                                                                                                131 A-----PVNGAYTANSROVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGA 183
                                                                                                                                                                                                                                                                                                                                                                                                                         184 TENYRPSFGSLADNPNHIAQFSSRG-ATRDGRIKPDVTAPGTFILSARSSLAPDSSFWAN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                          SGDQGWGRVTLDKSLNVAYVNEATALATG------QKATYSFQAQAGKPLKIS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 PFEQGSGRVQVDKAITQTVIAEPVSLSFGVQQWPHADDKPVTKKLTYRNLGTEDVTLKLT 532
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                                                                                                                                                                                                                                              GLYGQGQVVAVADFGLDFGRNDSSMHEAFRGKIFALYALGRTNNANDPNGHGTHVAGSVL 77
                                                                                                                                                                                                                      Gaps
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Jang H.J., Kim B.C., Pyun Y.R., Kim Y.S.;

A novel subtilistin-like serine protease from Thermoanserobacter
"A novel subtilistin-like serine protease from Thermoanserobacter
yonselensis KB-1: cloning, expression and biochemical properties.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                  75;
                                                                                                                                                                                       Length 1102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2] SEQUENCE FROM N.A.
Jang H.J., Kim B.C., Pyun Y.R., Kim Y.S.;
"Subtilisin-like protease, thermicin, from Thermoanaerobacter yonseii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermoanaarobacter yonseii.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
(VGBI_TaxID=111519)
                                                                                                                                                                                                                    Indels
                                                                                                                                                           F9E4AD2590FE559E CRC64;
                peptidolysis; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Thermidin (Subtilisin-like protease thermidin).
                                                                                                                                                                                       Query Match
15.4%; Score 347.5; DB 2;
Best Local Similarity 29.7%; Pred. No. 5.3e-12;
Matches 130; Conservative 52; Mismatches 181;
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GO; GO:0004289; F:subtilase activity; IEA
GO; GO:0006508; P:proteolysis and peptido
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                       InterPro; IPR002860, GH BNR.
InterPro; IPR002209; Peptidase_S8.
Ffam, PP002101; BNR; 2.
Ffam, PP00082; Peptidase_S8, 1.
FRINTS; PR00723; SUBTILISIN.
FROSITE; PS00136; SUBTILIASE_ASP; 1.
FROSITE; PS00138; SUBTILIASE_HSP; 1.
                                                                                                                                             Hydrolase; Protease; Serine_protease.
SEQUENCE 1102 AA; 114128 MW; F9E
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169 HVAGDAAGNGYASNGKYKGVAPEANIVAVKVLDSY----GRGSSSDILAGMOWVLDNKEK 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 YNIKİVSLSIGETPALPTF----LDPLVRGVDTLWKNGIVVVVAAGNSGPNYNSITSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 GTAKNAITVGATENYR-PSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 GTSRNAITVGAVDDKRIPDI-----EDDEVAKFSGRGGPY--LYKPDVVAPGVKIVSTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 SLAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 NNYGLYGOGOVVAVADTGLDTGRNDSSMHEAF---RGKITALY-ALGRINNANDPNGHGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HVAGSVLGN - ALN - - - KGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAW -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                         databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protease, Serine_protease.
412 Aa, 44503 MW, E3CGAOF81B1A1D47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.3%; Score 345.5; DB 2; 35.5%; Pred. No. 1.9e-12; ive 39; Mismatches 113;
                                                                                                                                                                           GO: GC:000823; F:peptidase activity; IEA.
GO: GO:0008289; F:subtilase activity; IEA.
GO: GO:0004289; F:subtilase activity; IEA.
GO: GO:0006508; P:protecolysis and peptidolysis;
InterPro: IPRO0209; Peptidase_S8.
PFINITS; PRO0723; SUBTILISIN.
PROSITE; PS00137; SUBTILISIN.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_HIS; 1.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8 EMBL, AYO28704; AAK27733.1; -. EMBL; AF305633; AAL09366.1; -. HSSP, Q45670; 1DBI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 AT---DVGLGYPSGDQGWGRVTLDKSL 315
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ATKINEAGL----WTQGSGMINIEEAL
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17;

Protease. T. yonsei Transglut Foreign p

Pyrococcu Hyperther

Protein e RP-III re Hyperther Protease.

F. balust Streptomy Pyrococcu WO9856926

Streptomy DhpA-mel

Aaw24122 Aaw94838 Aaw94838 Aaw94841 Abb09483 Aab1180 Aaw1366 Aaw13667 Aaw13668 Aaw13668 Aaw13668 Aaw1368 Aaw1368 Aaw1368 Aaw1368 Aaw1368 Aaw1484 Aaw94839 Aaw94839 Aaw94839 Aaw94839

Fragment

Run

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This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease A-1 from Bacillus sp NCIB12289 described in the method of the invention
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iive 0; Mismatches 0;
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Okuda M, Saeki K;
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12-APR-2001; 2001JP-00114048
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Saeki K;
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                                                                                  1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHBAPRGKITAIYALGRTN
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composition; oxidising agent.
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Score 2143; DB 5;
Pred. No. 1.5e-152;
9; Mismatches 9;
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                                             The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by claim acid and they have a high stability to oxidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 6-11; (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the enzyme to be an effective component of washing compositions including bleaches. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.)
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95.2%; Score 2143; DB 2;
Best Local Similarity 93.5%; Pred. No. 2.5e-152;
Matches 406; Conservative 19; Mismatches 9;
                 Disclosure; Page 58-63; 71pp; Japanese
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The invention relates to alkaline proceases produced by strains of Bacillus. The proceases ability to digest casein is not inhibited by cleid acid and they have a high stability to oxidising agents. The cleid acid and they have a high stability to oxidising agents. The is active over the pH range 4-13 and has at least 80% of its optimum cativity over the pH range 4-13 and has at least 80% of its optimum catable over the pH range 6-11; (b) after 30 minutes at 40 deg. C it is table over the pH range 6-11; (c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43;000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the component sense. The present sequence represents an alkaline protease. (Updated to 20-MAR-2003 to correct DR field.)
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                                                                                                                                           Kubota H,
                                                                                                                                                                                                                                                            Disclosure; Page 63-68; 71pp; Japanese.
                                                                                                                                           Saeki K,
                                                       98WO-JP004528
                                                                                   97JP-00274570
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nes 406; Conservative
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N-PSDB; AAX37279.
                                                                                                                                           Okuda M,
Nomura M
                                                                                                               (KAOS ) KAO CORP
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Shikata S,
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(KAOS ) KAO CORP.
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                                                                                                                                                                                                                                                                              07-OCT-1998;
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Matches 400;
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21-JUL-1999
                                                                                                                                                                                                                                                           15-APR-1999.
                                                                                                                                                                                                                 Bacillus sp.
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361
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                                                                                                                                                                                                                                                                                                                                                               detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease KP9860 from Bacillus sp strain XSM-KP9860 described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NDVARGIVKADVAQSSYGLYGGGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKORGITFKPSLLKAALIAGAADVGLGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKFLKISLVWSDAPASTSA
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                                                                                                                                                                                                                                                                                                              compositions
                                                                                                                                                                                                                                                           Sumitomo N;
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                                                                                                    Alkaline protease; detergent; laundry; bleaching; dishwasher.
                                                                                                                                                                                                                                                                                                                                                                                                                                               94.7%; Score 2130; DB 5; Length 434; 92.4%; Pred. No. 1.4e-151; rive 24; Mismatches 9; Indels (
                                                                               Bacillus sp KSM-KP9860 alkaline protease protein fragment
                                                                                                                                                                                                                                                                                                              detergent
                                                                                                                                                                                                                                                           Araki H,
                                                                                                                                                                                                                                                           Sato T,
                                                                                                                                                                                                                                                                                                             New modified alkaline proteases useful in
                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 12-13; 25pp; English.
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                                                                                                                                                                                                                                                           Kageyama Y,
                   AAM50081 standard; protein; 434
                                                                                                                                                                                                       22-NOV-2000; 2000JP-00355166.
12-APR-2001; 2001JP-00114048.
                                                                                                                                                                                   22-NOV-2001; 2001EP-00127851
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nes 401; Conservative
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Saeki K;
                                                                                                                                                                                                                                                                                        WPI; 2002-437518/47
                                                                                                                                                                                                                                      (KAOS ) KAO CORP
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 434 AA;
                                                                                                                                           EP1209233-A2.
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                                                           12-AUG-2002
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                                       AAM50081;
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Matches
           AAM50081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by olecacid and they have a high stability to oxidising agents. The alkaline protease of the invention has the following properties: (a) it settive over the pH range 4-13 and has at least 80% of its optimum estivity over the pH range 4-13 and has at least 80% of its optimum stable over the pH range 6-11; (b) afters 30 minutes at 40 deg. C it is stable over the pH range 6-11; (c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the blackness. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alkaline protease; Bacillus; casein digestion; oleic acid; enzyme; washing composition; oxidising agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alkali protease from Bacillus used in washing powders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hitomi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.3%; Score 2122; DB 2;
ilarity 92.2%; Pred. No. 9.5e-151;
Conservative 24; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 53-58; 71pp; Japanese.
                                                                                                                                                                                                                                                                                                                                    AAY17089 standard; protein; 639 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-JP004528,
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                                                                                                      434
                                                                                                                                                                  VPVGPONFSLAIVN 434
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(first entry)
                                                                                                      VPQGPQAFSLAIVN
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Nomura M;
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Peptide
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                                                                                               300
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                                                             TVGATENLIRPSFGSYADNINHVAQFSSRGPTXDGRIXPDVMAPGTYILSARSSLAPDSSF
                                                                                                                                                         SVTLVNDLDLVITAPNGTRYVGNDFSAPFDNNWDGRNNVENVFINSPQSGTYTIEVQAYN
AGARIHTINSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
             AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNERPNGGTISAPGTAKNAI
                                              TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                                                               WANHDSKYAYMGGTSMATPIVAGNVAQLREHPIKNRGITPKPSLLKAALIAGATDIGLGY
                                                                                                            446 WANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVGLGY
                                                                                                                                             PSGNGGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA
                                                                                                                                                                                            SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New modified alkaline proteases useful in detergent compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                             Alkaline protease; detergent; laundry; bleaching; dishwasher.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 20-21; 25pp; English
                                                                                                                                                                                                                                                                                                                              AAM50086 standard; protein; 433 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kageyama Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-2001; 2001EP-00127851.
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12-APR-2001; 2001JP-00114048.
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                                                                                                                                                                                                                                                                 VPVGPQNFSLAIVN 639
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Okuda M, Saeki K;
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                                            WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
                                                                                                                                                                                                 PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA
                                                                         AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
                                                                                                               TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                                                  Novel protease from Bacillus subtilis LC20 - useful in laundry and dishwashing detergents and for leather processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease; detergent; surfactant; leather processing; debittering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209. .64î
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "signal peptide"
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/note= "prepro region"
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                                                                                                                                                                                                                                                                                                                                                         AAW89547 standard; protein; 641
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                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus JP170 protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus sp.
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PSGNOGWGRVTLDKSLNVAFVNETSSLSTNOKATYSFTAQSGKPLKISLVWSDAPASTSA
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Best Local 9
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                    This is the amino acid sequence of a novel procease of Bacillus sp. JP170 (NCIB 12513), as deduced from the nucleotide sequence of an isolated gene (see BAN82392). The entire protein, including the signal peptide and prepro region, has 77% identity to alkaline procease Y (see AAM89548) from Bacillus. The invention provides vectors, recombinant host cells and methods for the recombinant production of the protease The protease is used in laundry and dishwashing detergents, for institutional and industrial cleaning, and for leather processing, as well as for debittering and enhancing the degree of hydrolysis of protein hydrolysates, for flavour development through hydrolysis of proteins degradation of undesired peptides and in enzymatic synthesis of peptides. It has enhanced stability towards oxidation under alkaline conditions, to towards bleaching agents of the protease activity is diminished. Such provides mutant cells in which the protease activity is diminished. Such cells can be used for the production of heterologous recombinant proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   casein digestion; oleic acid; enzyme;
                                                                                                                                                                                                                                                                                    ٦;
                                                                                                                                                                                                                                                        94.1%; Score 2116.5; DB 2; Length 641; 92.2%; Pred. No. 2.5e-150; ive 21; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease sequence from Bacillus species.
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Claim 7; Page 53-54; 77pp; English.
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Best Local Similarity
Matches 400; Conserv
                                                                                                                                                                                                                                  Sequence 641 AA;
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21-JUL-1999
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washing c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to alkaline proceases produced by strains of Bacillus. The proceases ability to digest casein is not inhibited by oleic acid and they have a high stability to exidising agents. The alkaline procease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the range pH 6-12; (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-11; (c) its isoclectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to exidising agents allows the enzyme to be an effective component of washing compositions including bleaches. The present sequence represents an alkaline protease of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bleaches. The present sequence represents an alkaline protease of invention. (Updated on 20-MAR-2003 to correct DR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kubota H, Hitomi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alkali protease from Bacillus used in washing powders
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    639
/note= "all residues indicated
acids"

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Location/Qualifiers
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                                                                                                                                                                                                                                                                              98WO-JP004528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okuda M,
Nomura M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-287736/27.
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         Key
Misc-difference 1
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This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38) compared to prior art alkaline proteases (31 and 32%). This sequence represents a fragment of the alkaline protease SD-521 from Bacillus sp strain SD-521 (FERM BP-11162) described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp SD-521 (FERM BP-11162) alkaline protease protein fragment.
                                                                                                                                                                                                                                                                                                             PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA
                                                                                                                                                                                                                                                                                                                                     SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVBVQAYN
                                                           AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
                                                                                       TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                                                                                                                                                    387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTXILSARSSLAPDSSF
                                                                                                                                                                                                                              WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
                                                                                                                                                                                                                                                    New modified alkaline proteases useful in detergent compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sumitomo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Кадеуаша У,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM50084 standard; protein; 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-NOV-2000; 2000JP-00355166.
12-APR-2001; 2001JP-00114048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPVGPQXFSLAIVN 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Okuda M, Saeki K;
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                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM50084;
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                        267
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    .640
/note= "all residues indicated as Xaa are arbitrary amino
acids"

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                                                                                                                                                                                                                                                                                                                                                    protease, Bacillus, casein digestion, oleic acid, enzyme,
composition, oxidising agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kageyama Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alkali protease from Bacillus used in washing powders
                                                                                                                                                                                                                                                                                                             An alkaline protease sequence from Bacillus species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 50-53; 71pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97JP-00274570
                                                                                                                                                                AAY17088 standard; protein;
                        434
                                                         VPVGPQXFSLAIVN 639
                                                                                                                                                                                                                                                 (revised)
(first entry)
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Matches 397; Conservative
                     VPQGPQAFSLAIVN
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Nomura M;
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Misc-difference
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21-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus sp.
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                                                                                                                                                                                                                                                                                                                                SYTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYTIEVQAYN 419
                                                                              NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS 120
                                                                                                                                                                                                                                                                                   proteases useful in
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                                                                                             AGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAI
                                                                                                                                                                                                                                      WANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGY
                                                                                                                                                                                                                                                                                                                   SVILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                                   1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN
                                                  NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                              AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
                                                                                                                                                                           TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                                                                                                                                                           TVGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSF
                                                                                                                                                                                                                        WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
                                                                                                                                                                                                                                                                     PSGNOGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA
             Gaps
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            Indels
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Pred. No. 1.2e-143;
8; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM50082 standard; protein; 433
ilarity 88.5%; Pro
Conservative 28;
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Saeki K;
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 Best Local Similarity
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            Matches
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(34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease E-1 from Bacillus sp strain D6-(FERM-P1592) described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGKIKPDVMAPGTFILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSGNGGWGRVTLDKSLNVAFVNETSSLSTNOKATYSFTAQSGKPLKISLVWSDAPASTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NANDPNGHGTHVAGSVLGNAL-NKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWN
                                                                                                                                                                                                                                                                                                                                     NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS
                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alkaline protease Y; detergent; surfactant; leather processing; debittering; flavour.
                                                                                                                                                                                         1;
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                                                                                                                                              Length 433;
                                                                                                                                                                                         Indels
                                                                                                                                              Query Match 89.8%; Score 2020.5; DB 5; Best Local Similarity 88.2%; Pred. No. 2.3e-143; Matches 383; Conservative 28; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVO NORDISK BIOTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00873479
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                                                                                                   Seguence 433 AA;
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This is the amino acid sequence of a Bacillus sp. alkaline protease Y that is said to have good alkali and surfactant resistance and improved detergency. It shows 77% identity to a newly isolated protease (see AAW89547) of Bacillus sp. UPI70 (NCIB 12213). The invention provides production of such proteases. The protease are used in laundry and chostwashing detergents, for institutional and industrial cleaning, and for leather processing, as well as for debittering and enhancing the degree of hydrolysis of protein hydrolysates, for flavour development through hydrolysis of proteins, degradation of undesired peptides and in enzymatic synthesis of peptides. They have enhanced stability towards oxidation under alkaline conditions, e.g. towards bleaching agents of the protease activity is diminished. Such cells can be used for the protease activity is diminished. Such cells can be used for the production of heterologous recombinant proteins
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dishwashing detergents and for leather processing
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                                                                         Claim 3; Page 55-56; 77pp; English
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                                                                                                                                    DNA coding alkali-protease Ya enzyme - has good alkali and surfactant resistance and improves detergency.
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methoxypolethyleneglycol; mPEG; skin; hair care product; cosmetic;
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                                                                                                                                                                                                                                                        2; Length
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Best Local Similarity 87.8%; Pred. No. 1.3e-142;
Matches 381; Conservative 30; Mismatches 22; Indels
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                                                                                                                                                                     Claim 2; Page 1; 17pp; Japanese.
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                                                                                                       WPI; 1992-288440/35
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                                                                                                                                                                                                                                     Sequence 433 AA;
                                                            28-NOV-1990;
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The present sequence represents the Bacillus lion Y protease. The invention claims for enzymes covalently modified on their surface by the ettachment of a large number of small polymentic molecules, e.g. the trachment of a large number of small polymentic molecules, e.g. the protein glycols (PEG). The polymentic molecules are coupled to the Netwinal amino group and the amino groups of lysine residues found on the surface of the enzyme. In the example given, the lion Y protease was modified using methoxypolethyleneglycol (mPEG) as the polyment molecule. The Netwinal amino group and the amino groups of the fourteen lysine residues present on the surface of the lion Y protease were modified. Modification of the enzymes increases the stability and/or reduces the sensitising potential (allergenicity) of the enzyme, without capacitising potential polymeric molecules, rather than a few very large ones, provides a more even effect with reduced activity loss. The modified on provides a more even effect with reduced activity loss. The modified cand hair care products, e.g. soaps, cosmettics, creams, gels, libsticks, hair gels, sun oils, shampoos, hair dyes, insect repellants, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New enzyme modified by attachment of many polymeric molecules - useful in skin and hair care products, has reduced tendency to cause sensitisation and increased stability.
                                                                                                                    /note= "The enzyme is modified by methoxypolethyleneglycol molecules covalently attached to the N-terminal amino group and to fourteen unspecified amino groups of lysine residues present on the surface of the enzyme"
  lipstick; hair gel; sun oil; shampoo; hair dye; insect repellant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; Page 44-45; 56pp; English.
                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                97DK-00000038.
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                                                                                 Key
Modified-site
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25-JUN-1997;
                                                                                                                                                                                                                         WO9830682-A1
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                                      Bacillus sp
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61 NASDPNGHGTHVAGSVLGNAL-NKGMAPQANLVFQSIMDSSGGLGGLPSNLNYLFSQAMN 119 240 61 NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS 120 121 AGARIHTINSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI 180 1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN 60 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF Gaps 7; 89.4%; Score 2010.5; DB 2; Length 433; 87.8%; Pred. No. 1.3e-142; Live 30; Mismatches 22; Indels 1; Conservative Query Match Best Local Similarity Matches 381; Conservat Sequence 433 AA; 엄 à g ò qq ð ò g

241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY 300

Db 240 WANTNSKYAMGGTGMATPILVAGNYAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGY 299

Qy 301 PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA 360

Db 300 PSGDGGMGRVTLDKSLNVAVNETALATGQKATYSFTAQSGKPLKISLVWBDAPASTSA 360

Qy 361 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVFINAPQSGTYTTEVQAYN 419

Db 360 SYTLVNDLDLVITAPNGGKYVGNDFSYPYDNNWDGRNNVFINAPQSGTYILEVQAYN 419

Qy 421 VPQGPQAFSLAIVN 434

Db 420 VPSGPQRFSLAIVN 434

Search completed: March 31, 2004, 16:04:33

Search completed: March 31, 2004, 16:04:33

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Appli Appl Appl Appli

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207 NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSWHEAFRGKITALYALGRTN
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93.5%; Pred. No. 2.7e-165;
live 19; Mismatches 9;
                           US-09-445-472-6
US-09-445-472-6
US-09-445-472-6
US-08-973-479-44
US-09-96-921A-2
US-07-76-921A-2
US-08-980-135-4
US-08-980-135-4
US-08-585-798-4
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APPLICANT: OKUDA, MIKIO
APPLICANT: OKUDA, MIKIOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIRONIA
APPLICANT: KAGEYANA, YASUSHI
APPLICANT: KAGEYANA, YASUSHI
APPLICANT: KAGEYANA, YASUSHI
APPLICANT: SHIKATA, SHITSUW
APPLICANT: SHIKATA, SHITSUW
APPLICANT: NOWURA, MASARUMI
APPLICANT: NOWURA, SHITSUW
APPLICANT: NOWURA, SHITSUW
APPLICANT: NOWURA: 0200-04-06
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT PILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VETSION 3.0
SSOFTWARE: PATENTIN VETSION 3.0
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Best Local Similarity 93.5'
Matches 406; Conservative
TYPE: PRT
, ORGANISM: Bacillus sp.
US-09-509-814A-6
.09-509-814A-6
327
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Copyright (c) 1993 - 2004 Compugen Ltd
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361 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420
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                                                                                                                                                                                       US-U9-509-814A-4

Sequence 4, Application US/09508814A

Patent No. 637627

GENERAL INFORMATION:
APPLICANT: TAKATWA, MIKIO
APPLICANT: CKUDA, MITSUYOSHI
APPLICANT: CKUDA, MITSUYOSHI
APPLICANT: KUBOTA, HIROMI
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: MONUTA, MASAFUMI
APPLICANT: MONBER: DCT/JP98/04528
FILE REFERENCE: 0327-0832-0PCT
CURRENT FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1997-06-08
NUMBER: OF SEQ ID NOS: 24
SEQ ID NO 4
LENGTH: 639
LENGTH: 639
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                                                                                                  627 VPVGPQNFSLAIVN 640
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                                                                              VPQGPQAFSLAIVN 434
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Best Local Similarity 92.2%;
Matches 400; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 NANDINGHGTHVAGSVLGNGSINKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                   SVILVNDLDLVITAPNGTKXVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAXN 420
                                                                                                                                                        567 SVILVNDLDLVITAPNGTQYVGNDFTSPYNDNWDGRNNVENVFINAPOSGTYTIEVQAYN 626
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                                                                                PIGNOGWGRVTLDKSLNVAYVNESSSLSTSQKATYSFTATAGKPLKI SLVWSDAPASTTA
                                                           PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAFASTSA
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TAKAIMA, MIKIO
APPLICANT: TAKAIMA, MITSUVOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: SAGEVAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUW
APPLICANT: SHIKATA, SHITSUW
APPLICANT: SHIKATA, SHITSUW
APPLICANT: NOWURA, MASAFUMI
TILE OF INNENTION: ALKALINE PROTEASE
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT FILING DATE: 1998-10-07
PRIOR PILING DATE: 1998-10-07
PRIOR PILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 8
SEQ ID NO 8
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09509814A Patent No. 6376227 GENERAL INFORMATION:
                                                                                                                                                                                                                                             627 VPVGPQTFSLAIVN 640
                                                                                                                                                                                                                  VPOGPOAFSLAIVN 434
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                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-509-814A-8
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568 SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAFQSGTYTVEVQAYN 627
361 SVILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: TAKANA, MIKIO
APPLICANT: SAEXI, KATSUHISA
APPLICANT: SAEXI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: SHIKATA, SHITSUM
APPLICANT: SHIKATA, SHITSUM
APPLICANT: SHIKATA, SHITSUM
APPLICANT: SHIKATA, SHITSUM
APPLICANT: MASAFUMI
ITILE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0327-0823-0PCT
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT FILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
CENCTHER DATE TO NOS: 24
CENCT DATE TO NOS: 24
CENCTHER DATE TO NOS: 24
CENCTHER DATE TO NOS

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DORATURE:

NAMES/KEY: misc feature

LOCATION: (23)... (23)

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc feature

LOCATION: (29)... (29)

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc feature

LOCATION: (32)... (32)

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc feature

LOCATION: (45)... (46)

OTHER INFORMATION: Xaa is any amino acid

NAMES/KEY: misc feature

LOCATION: (46)... (46)

OTHER INFORMATION: Xaa is any amino acid

NAMES/KEY: misc feature

LOCATION: (45)... (47)

OTHER INFORMATION: Xaa is any amino acid

NAMES/KEY: misc feature

LOCATION: (47)... (47)

OTHER INFORMATION: Xaa is any amino acid

NAMES/KEY: misc feature

LOCATION: (53)... (53)

OTHER INFORMATION: Xaa is any amino acid

NAMES/KEY: misc feature

LOCATION: (53)... (53)
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LOCATION: (89)...(89)
OTHER INFORMATION: Xaa is any amino acid
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NAME/KEY: misc feature
LOCATION: (128)..(128)
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INFORMATION: Xaa is any amino acid
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INFORMATION: Xaa is any amino acid
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THER INFORMATION: Xaa is any
                                                                                                                                                                        421 VPQGPQAFSLAIVN 434
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LOCATION: (70)..(70)
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LOCATION: (74)..(74)
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                                                                                                    US-088 873 479 42
US-088 873 479 42
US-088 873 479 42
Sequence 42, Application US/08873479
Patent No. 589701
GENERAL INFORMATION:
APPLICANT: Sloma, Alan
APPLICANT: Lynne, Christianson
ITILE OF INVENTION: Mucleic Acids Encoding A Polypeptide
ITILE OF INVENTION: Maying Protease Activity
CORRESPONDENCES: 57
CORRESPONDENCE ADDRESS:
ACOUNTER: New York
STATE: Distribution
SOUTHARD FREADABLE FORM:
MEDIUM TYPE: IS-087410N
SOUTHARE: FREADABLE FORM:
MUCLE STATEN NUMBER: 34,086
REFERENCE/ONCKET NUMBER: 34,086
REFERENCE/ONCKET NUMBER: 5251.000-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATIO
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INFORMATION: Xa.	/KEY: misc featur FION: (130)(130 R INFORMATION: Xa /KEY: misc featur	INFORMATION: Xa	ION: (132)(132 INFORMATION: Xa KEY: misc_featur	: (133)(133 FORMATION: Xa : misc featur	ION: (146)(146) ION: Xa	TION: (148)(148 R INFORMATION: Xa	ION: (160)(160 INFORMATION: Xa	ION: (165)(165 INFORMATION: Xa	ION: (172)(172 INFORMATION: Xa	ION: (183)(183 INFORMATION: Xa	. (187 N: Xa	ION: (188)(188 INFORMATION: Xa	INFORMATION: Xa(EY)	ION: (194)(194 INFORMATION: Xa	TION: (286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(286)(2	TION: (306)(306) RINFORMATION: Xa	: (324) . (324 FORMATION: Xa : misc featur	rion: (369)(369 R INFORMATION: Xa /KEY: misc featur	rion: (431)(431 R INFORMATION: Xa /KEY: misc_featur	TION: (501)(501 R INFORMATION: Xa /KEY: misc featur	TION: (531)(531 R INFORMATION: Xa /KEY: misc_featur	(541) (541 ORMATION: Xa	Intervention of the control of the c	i: misc reac N: (591)(S NFORMATION:

ö 325 240 445 505 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420 206 NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 265 61 NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS 120 180 WANHDSKYAYMGGTSWATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY 300 PSGNQCWCRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA 360 9 446 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADXGLGY 121 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI 1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN TVGATENLRPSFGSYADNINHVAQFSSRGPTXDGRIKPDVMAPGTFILSARSSLAPDSSF Gaps . 0 Length 639; Indels Query Match 92.5%; Score 2082; DB 4; Best Local Similarity 91.5%; Pred. No. 2.4e-160; Matches 397; Conservative 14; Mismatches 23; Sequence 2, Application US/09509814A
Patent No. 637627
GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIXIO
APPLICANT: SAEKI, KATSUHISA
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: SHIXATA, SHITSUM
APPLICANT: SHIXATA, SHIXINE
THILE OF INVENTION: ALKALINE
TILLE OF INVENTION: ALKALINE
TILLE OF INVENTION: ALKALINE
CURRENT APPLICATION NUMBER: US/09/509,814A COCATION: (592)...(592)
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (594)...(594)
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (595)...(595)
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
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US-09-509-814A-1 VPOGPOAFSLAIVN 434 VPVGPQXFSLAIVN 639 RESULT 6 US-09-509-814A-2 301 . 979 181 241 909 361 421 셤 ò d ð g ૪ 임 δ g ò g ò d  $\stackrel{\circ}{\sigma}$ g ò

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CURRENT FILING DATE: 2000 PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR PILING DATE: 1997-06 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin version SOFTWARE: Patentin version LENGTH: 640 TYPE: PRT PRATIER: PRATIER: PRATIER:	: misc fe : (3) . (5) FORMATION	(24)(24) DRMATION: misc_feat (30)(30) DRMATION:	(33) (33) ORMATION: Xa misc_featur (47) (47)	ATION: sc_feat 8)(48	ORMATION: misc_feat (54)(54	INFORMATION: XEY: misc_feat ION: (71)(71	RMATION: misc_fea (75) (7	RMATION: misc feat	ON: (90)(90) INFORMATION: Xa EY: misc_featur	(103)(103)RMATION: Xa	(106)(106)RMATION: Xa	(129)(129)RMATION: Xamisc featur	(131) (131) FORMATION: Xa : misc featur	ION: (132)(132) INFORMATION: Xa ŒY: misc_featur	FION: (133)(133) R INFORMATION: Xaa i /KEY: misc feature	: (134)(134) FORMATION: Xaa i : misc feature	TION: (147)(147) R INFORMATION: Xaa i /KEY: misc_feature	CATION: (149)(149) HER INFORMATION: Xaa i ME/KEY: misc_feature	(161)(161) ORMATION: Xaa i misc_feature

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)(166 ION: Xa featur	)(173 ION: Xa featur	)(184 ION: Xa featur	)(188 ION: Xa feathr	(189 ION: Xa	7. (190 ION: Xa	(195 ON: Xa	) (287 ION: Xa	7. (307 ION: Xa	7. (325 ION: Xa	reatur 7(370 ION: Xa	reatur 7(432 ION: Xa	featur 7(502 ION: Xa	featur 7(532 ION: Xa	featur 7(542 ION: Xa	featur 7(585 ION: Xa	featur 7. (592 ION: Xa	featur )(593	featur	ION: Xa featur	)(596 ION: Xa_ _featur_	)(597 ION: Xa featur	)(612 ION: Xa featur	TION: (633)(633 R INFORMATION: Xa 9-814A-2
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Query Match
92.5%; Score 2082; DB 4; Length 640;
Best Local Similarity 91.5%; Pred. No. 2.4e-160;
Matches 397; Conservative 14; Mismatches 23; Indels 0

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Sequence 4, Application US/09019532B Patent No. 6416756
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TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
STRAIN: Bacillus sp.
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           ; TOPOLOGY:
; MOLECULE TYPE;
; ORIGINAL SOUR
; STRAIN: BE
US-09-104-623A-4
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CITY: NAW YORK
STREET: 405 Lexington Avenue
CITY: NAW YORK
STREET: BN COMPUTER: NAW
COUNTRY: USA
ZIF: 10.74
COMPUTER: BM COMPACIBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: BM COMPACIBLE
COMPUTER: BM COMPUTER: BM COMPA
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                                                          207 NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRYN 266
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                             NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN
                                                                                                                                    NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVPQSVMDSNGGLGGLPSNVSTLFSQAYS
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APPLICANT: Patum, Tine Muxoll
APPLICANT: Deussen, Heinz-Josef
APPLICANT: Reggen, Erwin Ludo
TITLE OF INVENTION: A Modified Polypeptide
CORRESPONDENCE: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 2007-
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TYPE: amino d
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NASDPNGHGTHVAGSVLGNAL-NKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420
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4; Length 433;
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ADPLICANT: Olsen, Arne Agerlin
APPLICANT: Prent , Arnette
TITLE OF INVENTION: A Modified Enzyme for Skin Care
FILE REPERENCE: 4922.204-US
CURRENT APPLICATION NUMBER: US/99/019,532B
CURRENT FILING DATE: 1998-02-05
EARLIER FILING DATE: 1997-01-10
EARLIER FILING DATE: 1997-01-10
EARLIER FILING DATE: 1997-01-10
EARLIER FILING DATE: 1997-00-05
EARLIER FILING DATE: 1997-00-05
EARLIER FILING DATE: 1997-00-07
EARLIER FILING DATE: 1998-01-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
FOUNDER OF SEQ ID NOS: 5
SEQ ID NO 4
FOUNDER OF SEQ ID NOS: 5
FOUNDER OF
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89.4%; Score 2010.5; DB 4;
Best Local Similarity 87.8%; Pred. No. 8.4e-155;
Matches 381; Conservative 30; Mismatches 22;
Query Match

89.4%; Score 2010.5; DB 4.
Best Local Similarity 87.8%; Pred. No. 8.4e-155;
Matches 381; Conservative 30; Mismatches 22;
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361 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420
                                                                                                                                                                                                                                                                                         SYTLVNDLDLVITAPNGQKYYGNDFSYPYDNWWDGRNNVENVFINAPQSGTYIIEVQAYN 419
20 AGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAI 179
                                                                                                                                                                                                           300 PSGDQGWGRVTLDKSLNVAYVNBATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTA
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                                     TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                         241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
                                                                                                                                     240 WANYNSKYAYMGGISMAIPIVAGNVAQLREHFIKNRGIIPKPSLIKAALIAGAIDVGLGY
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APPLICANT: Slow, Alan
APPLICANT: Slow, Christianson
TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
CORRESPONDESS:
ADDRESSEE: No. 5891701 No. 5891701disk of No. 5891701th America
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
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llarity 87.8%; Pred. No. 1.4e-154;
Conservative 30; Mismatches 22;
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COMPUTER: IBM Compatible
OMPATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,479
FILING DATE: 12-UNH 1997
CLASSIFICATION: 530
ATTORNEY AGENT INPORMATION:
NAME: AGISTRATION NUMBER: 34,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 5251.000-US TELECOMMUNICATION: TELEPHONE: 212-867-0123
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US-08-873-479-43
Sequence 43, Application US/08873479
Patent No. 5891701
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acids
TYPE: amino acid
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120 VPSGPQRFSLAIVH 433
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity
Matches 381; Conserval
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US-08-873-479-43
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                                       NDVARGIVKADVAQNNYGLYGQQQLVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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87.8%; Pred. No. 8.4e-155;
ive 30; Mismatches 22; Indels
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Patent No. 663826
GENERAL INFORMATION:
APPLICANT: Deutsen, Heinz-Josef
APPLICANT: Cléen, Arne A.
APPLICANT: Reggen, Erwin L.
TITLE OF INVENTION: A Polypeptide-Polymer Conjugate
FILE REPERBRÜCE: 5649.200-US
CURRENT APPLICATION NUMBER: US/09/338,746
CURRENT PILING DATE: 1999-06-23
EAALIER APPLICATION NUMBER: EA 1998 00809
EAALIER APPLICATION NUMBER: 60/091,461
EAALIER FILING DATE: 1998-07-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 87.84
Matches 381; Conservative
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US-09-338-746-4
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US-09-338-746-4
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241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY 300
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US-09-196-281-13
Sequence 13, Application US/09196281A
Sequence 13, Application US/09196281A
Sequence 13, Application US/09196281A
SAPPLICANT: Hansen, Peter K.
APPLICANT: BANGIZ, Peter K.
APPLICANT: Mikkelsen, Frank
TITLE OF INVENTION: Protease Variants And Compositions
FILE REPRENCY: 5435.200-US
CURRENT APPLICATION NUMBER: US/09/196,281A
CURRENT APPLICATION NUMBER: 132/97
EARLIER FILING DATE: 1990-11-19
SARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 18
SOFFWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                    Sequence 10, Application US/09515150A

Sequence 10, Application US/09515150A

Sequence 10, Application US/09515150A

Setent No. 655898

GENERAL INFORMATION:

APPLICANT: Hansen, Peter

APPLICANT: Mikkelen, Frank

CURRENT: APPLICANTON: Protease Variants and Compositions

CURRENT APPLICATION NUMBER: US

CURRENT APPLICATION NUMBER: US

CURRENT FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Version 3.1

SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
69.4%; Score 1562.5; DB 4;
Best Local Similarity 92.5%; Pred. No. 1.1e-118;
Matches 294; Conservative 16; Mismatches 7;
                                                           PNGNQGWGRVTLDKSLNV 345
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US-09-515-150A-10
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                                                                                                                                                                                                                   TVGATENYRPSFGSIADNPWHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSF
                         PSGDQGWGRVTLDKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTA
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NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVPQSVMDSNGGLGGLPSNVSTLFSQAYS
                                                                                          AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
                                                                                                                                     AGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAI
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69.4%; Score 1562.5; DB 4; Length 345;
Best Local Similarity 92.5%; Pred. No. 1.1e-118;
Matches 294; Conservative 16; Mismatches 7; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-512-51A-10

S-09-512-51A-10

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S-09-512-51A-10

S-09-512-51A-10

Patent No. 655535

GENERAL INPORMATION:
APPLICANT: Bauditz, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelsen, Frank
APPLICANT: Andersen, Kim
ITILE OF INVENTION: Protease Variants and Compositions
FILE REPREBRUCE: 5349.204-US
CURRENT APPLICATION NUMBER: US/09/512,251A

CURRENT APPLICATION NUMBER: US/09/512,251A

CURRENT FILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 10

LENGTH 245
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ORGANISM: Bacillus
US-09-512-251A-10
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Sequence 1, Application US/08894818B

Patent No. 6261822

GENERAL INFORMATION:
APPLICANT:
APPLICANT: MORISHITA, Mio
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: TSUNASAMA, Susumu
APPLICANT: TSUNASAMA, Susumu
APPLICANT: TSUNASAMA, Susumu
APPLICANT: TSUNASAMA, Susumu
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, SUSUMU
APPLICANT: ASADA, SUSUMU
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, SUSUMU
APPLICANT: ASADA, KIYOZO
CORRESONDRICE ADDRESS:
ADDRESSEB: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
CITY: Washington
ZIP: COUNTRY: United State.
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MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin NOMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
CLASSIFICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION NUMBER: DCT/D96/03253
RICK APPLICATION NUMBER: JP 323285/1995
RILING DATE: 12-DEC-1995
ATTONENY-AGENT INFORMATION:
NAME: APCACL.
                                                                                                                      Query Match
69.4%; Score 1562.5; DB 4;
Best Local Similarity 92.5%; Pred. No. 1.1e-118;
Matches 294; Conservative 16; Mismatches 7;
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: United States of America
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REGISTRATION NUMBER:
                  TYPE: PRT
ORGANISM: Bacillus
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US-08-894-818B-1
                                                 ; ORGANISM: Bac
US-09-196-281-13
LENGTH: 345
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Sequence 12, Application US/09445472

Patent No. 6358726

GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: HUMOJO, Tomoko
APPLICANT: KATO, Ikunoshin
ITLEO PO INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKURA=6
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US/09/445,472
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR PILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin version 3.0

LENGTH: 659
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REFERENCE/DOCKET NUMBER: TAKAKURA=1
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: alloar
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: TYPE: peptide
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                                                                                          242 ANHDSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITP---KPSLLKAALIAGATDIG- 297
                                                                                                                                                                                                                                                                                                                                                                       365 TPINDYYTKASGTSMATPHVSGVGALILQ---AHPSWTPDKVKTALIETADIVAPKEIAD 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 PASTSASVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTV 414
                                                                                                                                         67 GHGTHVAGSVLGNGTSNK---GMAPQANLVFQSVM--DSNGGLGGLPSNVSTLFSQAYSA 121
                                                                                                                                                                                                            122 GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAIT 181
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                                                                      8 VKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIY-ALGRINNANDFN 66
                                   63; Gaps
Length 659;
Query Match

20.0%; Score 450.5; DB 4; Length 6
Best Local Similarity 31.4%; Pred. No. 3.1e-28;
Matches 138; Conservative 69; Mismatches 170; Indels
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518 KVVSY---KGAANYQVDVVS 534
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Search completed: March 31, 2004, 16:11:56 Job time : 15.0215 secs

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March 31, 2004, 16:09:09; Search time 33.2177 Seconds (without alignments) 3418.697 Million cell updates/sec
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1 NDVARGIVKADVAQSSYGLY.........EVQAYNVPQGPQAFSLAIVN 434
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 6, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 10, Appl	Sequence 13, Appl	Sequence 12, Appl	Sequence 1, Appli	Sequence 4, Appli	Sequence 16, Appl	Sequence 13251, A
SUMMARIES	ДІ	US-09-985-689A-6	US-09-985-689A-1	US-10-385-662-2	US-09-985-689A-2	US-09-985-689A-7	US-09-985-689A-5	US-09-985-689A-3	US-09-985-689A-4	US-10-336-324-10	US-10-403-105-13	US-10-090-624-12	US-10-090-624-1	US-10-090-624-4	US-10-090-624-16	US-10-156-761-13251
	DB	107	10	12	10	10	10	10	10	14	14	13	13	13	13	14
	l Query Match Length	434	434	434	434	433	433	433	433	345	345	629	412	522	654	1208
di	Query Match	100.0	95.2	95.2	94.7	94.1	90.0	89.8	89.1	69.4	69.4	20.0	18.0	18.0	18.0	16.1
	Score	2250	2143	2143	2130	2116.5	2024.5	2020.5	2005.5	1562.5	1562.5	450.5	404	404	404	362
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61 NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS 120

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1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN

Query Match
Best Local Similarity 100.0%; Pred. No. 3e-189;
Matches 434; Conservative 0; Mismatches 0; Indels 0;

Sequence 39, Appl Sequence 4, Appli Sequence 6, Appli Sequence 114, Appli Sequence 59, Appli Sequence 52, Appli Sequence 1234, A Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 1, Appli Sequence 3, Appli Sequence 6, Appli	
US-10-112-498-39 US-10-112-498-39 US-10-116-455-4 US-10-314-657-4 US-10-090-624-6 US-10-090-624-6 US-10-090-624-6 US-10-094-84624-114 US-09-927-827-55 US-09-927-827-55 US-09-927-827-55 US-09-927-827-55 US-10-156-761-12934 US-10-242-549-60	ALIGNMENTS 985689A Al II II II II IV 105/09/985,689A 7-01 P2000-355166 2 P2001-114048
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                                                                                            301 PSGNOGWGRVTLDKSLNVAPVNETSSLSTNOKATYSFTAQSGKPLKISLVWSDAPASTSA 360
                                                                                                                                                                            SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420
                                                                                                                                                                                                                                                 361 SVTLVNDLDLVITAPNGTQYVGNDFTSPYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 420
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TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240
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                        241 WANHDSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
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Best Local Similarity 93.5%; Pred. No. 7.9e-180;
Matches 406; Conservative 19; Mismatches 9;
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US-10-385-662-2
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  61 NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAXS 120
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                                                             AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
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Best Local Similarity 93.5%; Pred. No. 7.9e-180;
Matches 406; Conservative 19; Mismatches 9;
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Publication No. US20030022351A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GARAA, YUJI
APPLICANT: GARAA, YUJI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, ATSUYOSHI
APPLICANT: SUNITONO, NOBUTUKI
APPLICANT: SUNITONO, NOBUTUKI
APPLICANT: SUNITONO, NUMBER: US/09/985,689A
TITLE OF INVENTION: Alkaline proceases
TILLE OF INVENTION: Alkaline proceases
TILLE OF INVENTION: Alkaline proceases
TILLE OF INVENTION SATORER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: UP P2001-114048
PRIOR FILING DATE: 2001-04-12
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                                                                                            300 PNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA 359
301 PNGNQGWGRVTLDXSLNVAYVNESSALSTSQKATYTFTATAGKPLKISLVWSDAPASTTA 360
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                                                          361 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
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92.2%; Pred. No. 1.7e
iive 21; Mismatches
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US-09-985-689A-7
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Best Local Similarity
Matches 400; Conserva
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                                                                                                                                                                                  361 SVTLVNDLDLVITAPNGTQYVGNDFTSPYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 420
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                                                                                241 WANHDSKYAYMGGISMAIPIVAGNVAQLREHFVKNRGIIPKPSLLKAALLAGAADIGLGY
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                                     241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
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94.7%; Score 2130; DB 10;
Best Local Similarity 92.4%; Pred. No. 1.1e-178;
Matches 401; Conservative 24; Mismatches 9;
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Publication No. US20030022351A1
GENERAL INFORMATION:
APPLICANT: HORDANTION:
APPLICANT: ACREYAM, AKINORI
APPLICANT: ARGEYAM, ASUGHI
APPLICANT: ARGEYAM, ASUGHI
APPLICANT: SATO, TEUYOSHI
APPLICANT: SATO, TEUYOSHI
APPLICANT: SANITON, NOBUTUKI
APPLICANT: SANITON, AIKAINE
APPLICANT: SANITON, AIKAINE
APPLICANT: SAEXI, KATSUHISA
ITILE OF INVENTION: AIKAINE PROCESSES
FILE REFERENCE: 215483US
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
IEBNGTH: 434
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ORGANISM: Bacillus sp
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GENERAL INFOCRATION:
APPLICANT: GARA, YUJI
APPLICANT: GARA, AKINORI
APPLICANT: GAGSTANA, YSAUSHI
APPLICANT: SATO, TSUTOSHI
APPLICANT: SATO, TSUTOSHI
APPLICANT: SUMITOWO, NOBUYUI
APPLICANT: OKUDA, MITSUTOSHI
APPLICANT: SUMITOWO NOBUYUI
APPLICANT: OKUDA, MITSUTOSHI
APPLICANT: OKUDA, MITSUTOSHI
FILE REFERENCE: 215483USO
CURRENT FILING DATE: 2002-07-01
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
NUMBER: OF SEQ ID NOS: 7
SEQ ID NOS: 7
SEQ TWARE: PATENTIN VERSEN: 311
SEQ ID NOS: 7
     Publication No. US20030022351A1
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                                                                                                                                                                                                            APPLICANT: HATADA, YUJI
APPLICANT: GGAMA, AKINORI
APPLICANT: GAGYA, YASUSHI
APPLICANT: SATO, TSUYGSHI
APPLICANT: SATO, TSUYGSHI
APPLICANT: SUNITOMO, NOBUYKI
APPLICANT: SUNITOMO, NOBUYKI
APPLICANT: SUNITOMO, ALKALINE APPLICANT: SAEKI, KATSUHISA
TITLE REPERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: UP P2000-355166
PRIOR APPLICATION NUMBER: UP P2001-114048
PRIOR APPLICATION NUMBER: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR PRILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
                                                                                                                                           Sequence 5, Application US/09985689A Publication No. US20030022351A1 GENERAL INFORMATION:
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420 VPVSPQTFSLAIVH 433
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ORGANISM: Bacillus sp
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                                                                                                    Length 433;
                                                                                                                                                     22; Indels
                                                                                                    DB 10;
                                                                                                  89.8%; Score 2020.5; DB 10
88.2%; Pred. No. 4.7e-169;
tive 28; Mismatches 22;
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Publication No. US20330022351A1
GENERAL INFORMATION:
APPLICANT: HATPADA, YUUI
APPLICANT: OGAWA, AKINORI
APPLICANT: SAGEYAMA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HROYUKI
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                                                                                               Query Match
Best Local Similarity 88.2%
Matches 383; Conservative
) TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-3
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RESULT 7 US-09-985-689A-3 ; Sequence 3, Application US/09985689A

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Indels
                                                                                                                                Query Match 69.4%; Score 1562.5; DB 14;
Best Local Similarity 92.5%; Pred. No. 6.6e-129;
Matches 294; Conservative 16; Mismatches 7;
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, Sequence 13, Application US/10403105
; Publication No. US20030180933A1
; GENERAL INFORMATION:
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              ; SEQ ID NO 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Bacillus
US-10-336-324-10
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) Sequence 10, Application US/10336324
) Publication No. US20030176304A1
) General INFORMATION
) APPLICANT: Handen, Peter
) APPLICANT: Bauditz, Peter
) APPLICANT: Mikkelsen, Frank
APPLICANT: Mikkelsen, Frank
APPLICANT: Mikkelsen, Rim
ITLE OF INVENTION: Procease Variants and Compositions
FILE REFERENCE: 5349-204-03
FILE REFERENCE: 5349-204-03
PRIOR APPLICATION NUMBER: US/09/512,251A
PRIOR FILING DATE: 2000-02-24
) NUMBER OF SEQ ID NOS: 12
) SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.6%; Pred. No. 9.8e-168;
Matches 380; Conservative 31; Mismatches 22;
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: OKUDA, MITSUTOSHI
APPLICANT: OKUDA, MITSUTOSHI
APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: Alkaline proteases
FILE REFERENCE: 215483USO
CURRENT PAPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: JP P2000-355166
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN DATE: 2010-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
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ORGANISM: Bacillus sp.
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US-10-336-324-10
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                                                                                                                                                         29 NDVARGIVKADVAQNNFGLYGQGQIVAVADIGLDIGRNDSSMHEAFRGKITALYALGRTN
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                                                                                                                    1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN
                                                            1; Gaps
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APPLICANT: Handlitz, Peter K.
APPLICANT: Bauditz, Peter K.
APPLICANT: Mikkelsen, Frank
ITILE OF INVENTION: Protease Variants And Compositions
FILE REFERENCE: 5435.200-US
GURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US/09/196,281A
PRIOR APPLICATION NUMBER: US/09/196,281A
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1332/97
PRIOR RILING DATE: 1998-11-19
PRIOR RILING DATE: 1998-11-19
PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 345
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DB 14; Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 HINSWGAPVNGAYIIDSRNVDDYVRKNDMAVLFAAGNEGPNGGIISAPGIAKNAIIVGAI 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 INLSLGSSQSSDGTDALSOAVNAAWDAGLVVVVAAGNSGPNKYTIGSPAAASKVITVGA-
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                                                                                                                                                                                                                        APPLICANT: TAKAKURA, Hikaru
APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: KAYO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REPERENCE: TAKAKURA=6
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT PILING DATE: 2002-06
PRIOR PLING DATE: 1997-12-06
PRIOR PLING DATE: 1997-10-10
PRIOR PLING DATE: 1997-06-10
NUMBER: OF SEQ ID NOS: 33
SOFTWARE: PACENTIN VERSION 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 412;
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         434
                                    :|::|::|:
518 KVVSY---KGAANYQVDVVS 534
                                                                                                                                                           Sequence 1, Application US/10090624; Publication No. US20020132335A1; GENERAL INFORMATION:
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Publication No. US20020132335A1
GENERAL INFORMATION:
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                                                                      67 GHGTHVAGSVLGNGTSNK---GMAPQANLVFQSVM--DSNGGLGGLPSNYSTLFSQAYSA 121
                                                                                                                                 241 WANHDSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSILKAALIAGATDIGLGY 300
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148 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 GIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAAASKVIT
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Sequence 12, Application US/10090624
Sequence 12, Application US/10090624
Sequence 12, Application Wo. U320020132335A1
GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: ARADA, Kiyozo
APPLICANT: ARADA, Kiyozo
APPLICANT: ARADA, Kiyozo
APPLICANT: ARADA, Kiyozo
APPLICANT: ARADA, US/2000-601
TITLE OF INVENTION: 285TEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKURA-6
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-06-10
NUMBER: OF SEQ ID NOS: 33
SOFTWARPE: DEFORMATION NOSE: 33
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; Pred. No. 1.2e-30;
69; Mismatches 170; Indels
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Best Local Similarity 31.4%;
Matches 138; Conservative 69
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; ORGANISM: Thermococcus celer
US-10-090-624-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 ENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWANHD 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGNOGWGRVTLDKSL---NVAFVNETSSLSTNOKATYSFTAQSGKPLKISLVWSDAPAST 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74;
APPLICANT: MOSISHITA, Mio

APPLICANT: MASISHITA, Mio

APPLICANT: ASADA, Kiyozo

CURRENT APPLICATION NUMBER: US/10/090,624

CURRENT APPLICATION NUMBER: US/10/090,624

PRIOR PILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1997-06-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN VEXEION 3.0

SEQ ID NO 4

LENGTH: 522
                                                                                                                                                                                                                                                                                                                                                                                                                                             query Match
Best Local Similarity 30.0%; Pred. No. 1e-26;
Matches 131; Conservative 63; Mismatches 168: Trdel 7
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Publication No. US20020132335A1
GENERAL INFORMATION:
APPLICANT: TAKAKIRA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: SHIMOJO, Tomoko
APPLICANT: ASADA, KYYOZO
APPLICANT: KAJO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
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LOCATION: (428)...(428)

LOCATION: (428)... (428)

US-10-090-624-4
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ORGANISM: Pyrococcus furiosus
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US-10-090-624-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 GYDGSGITIGIIDTGID-----ASHPDLQGKV----IGWVDFVNGRSYPYDDHGHGTH
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Publication No. US2030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAMA, JUN
APPLICANT: ISHIKAMA, JUN
APPLICANT: SHIBA, TADAVOSHI
APPLICANT: SHIBA, TADAVOSHI
APPLICANT: SAKKI, YOSHIVKI
APPLICANT: APTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT FILE DEPENST 249-262
CURRENT FILE OF SERENCE: 249-265-29
FRIOR PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILEGO DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PLING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
CURRENT APPLICATION NUMBER: US/10/090,6
CURRENT FILING DATE: 2002-03-06
FRIOR APPLICATION NUMBER: 09/445,472
FRIOR PILING DATE: 1999-12-06
FRIOR FILING DATE: 1999-12-06
FRIOR FILING DATE: 1997-06-10
FRIOR FILING PATE: 1997-06-10
FRIOR FILING PATE: 1997-06-10
FRIOR FILING PATE: 1997-06-10
FRIOR FILING PATE: 1997-06-10
FRIOR FILING FIL
                                                                                                                  US/10/090,624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pyrococcus furiosus US-10-090-624-16
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Best Local Similarity
Matches 131; Conserva
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US-10-156-761-13251
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Query Match
16.1%; Score 362; DB 14; Length 1208;
Best Local Similarity 30.1%; Pred. No. 1.7e-22;
Matches 135; Conservative 62; Mismatches 186; Indels 66; Gaps 17;
                                                                                                                                                                                                                                                            240 DGEEVADRNGHGTHVTSTVGGSGAASDGTERGVAPGATLAVGKVL-SDQGAGSESQIIAG 298
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                                                                                                                                                                                                                                                                                                         114 LFSQAYSAGARIHTNSWGAPVNGAYTTD--SRNVDDYVRKNDMAVLFAAGNEGPNGGTIS 171
                                                                                                                                                                     8 VKADVAQSS------YGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALG 57
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; SEQ ID NO 13251
; LENGTH: 1208
; TYPE: PRT
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multidrug resistance transport protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18279
R;Shaulsky, G.; Loomis, W.F.
R;Shaulsky, G.; Loomis, W.F.
R;Shaulsky, G.; Loomis, W.F.
A;Reference number: 218855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 SAGARIHTNSWGA----PVNGAYTIDSRNVDDYVRKN-DMAVLFAAGNEGPNGGIIS--A 172
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DAGARVHCDSWGSVSVEGYTGSYSSDTASIDDFLFTHPDFIILRAAGN---NEQYLSLLT
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23.0%; Score 518.5; DB 2;
Best Local Similarity 28.0%; Pred. No. 6.3e-25;
Matches 165; Conservative 77; Mismatches 155;
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A33973
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(c) 1993 - 2004 Compugen Ltd.
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intracellular alkaline serine proteinase aprX - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: A69587
C;Accession: A69587
C;Accession: A69587
C;Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B.; Alloni, G.; Azevedo, V.; Berre
R;Kunst, F.; Ogsaswara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berre
C; Bron, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capueno, V.; Carter, N.M.; C.
A; Enrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Funa, S.; Galizzi, B.;
A; Enrlich, S.D.; Emmerson, P.T.; Hilbert, H.; Holseppel, S.; Fubret, C.; Ferrari, B.
A;Authors: Foulger, D.; Fritz, C., Fujita, M.; Kurita, K.; Lapidus, A.; Hardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y, M.; Ogswa, K.; Ogiwa, R.; Oddega, B.; Park, S.H.; Parro, V.; Posttell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Sadaie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schreeter, R.; Scoffone, F.; Sekfguchi, J.; Sato, T.; Scanlon
A;Authors: Schleich, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Udiiyama
T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-postive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:930437.
   intracellular alkaline serine proteinase aprX [imported] - Bacillus halodurans (strain intracellular alkaline serine proteinase aprX [imported] - Bacillus halodurans (space: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 R.Jaccasion: B83891 R.Ja
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llarity 31.8%; Pred. No. 1.2e-14;
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multidrug resistance protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Becies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18267
R;Shaulsky, G; Kuspa, A.; Loomis, W.F.
R;Shaulsky, G; Kuspa, A.; Loomis, W.F.
R;Shaulsky, G; Kuspa, A.; Loomis, W.F.
A;Description: An MDR transporter/Serine protease gene is required for prestalk
A;Reference number: 218850
A;Recession: T18267
A;Accession: T18267
A;Accession: T18267
A;Accession: T18267
A;Accession: DAA
A;Residues: 1-1905 <SHA>
A;Across references: EMBL:U20432; NID:g664839; PID:g664840; PIDN:AAA62212.1
C;Genetics:
A;Genetics:
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----AQSGKPLK---ISLVWSDAPASTSASVTLVNDLDLVITAPNGTKYVGNDFTAPYD 390
                                                        785 PSSSSSNSGNNIPRVVATLVMTDPPSYAGAKFNLVNNLDLTM----IYYRDNGSTIFYS 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
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DAGARVHGDSWGSVSLQGYYGGYSDDAGIDAFLYEYPEFSILRAAGN-NELFASILAQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYGOGQVVAVADTGLDTGR---NDS----SMHEAFRGKITAIYALGRTNNANDP--N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1905;
                                                                                                                                                                 840 NOGGSSFLGLAPTODILNNVEGIVENPTEPMTYRFMVAGTNVPMGPQNFS
                                                                                                                      N------NWDGRNIVENVFINAPQSGTYTVEVQAYNVPQGPQAFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GITPKPSLLKAALIAGATDIGLGY-----PSGN---
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Best Local Similarity
Matches 132; Conserv
                                                                                                                                                                                                                                                                   A; Residues: 1-806 < KUN>
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A.Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, V.; Funa, S.; Galizzi, A.; Galler Je, H. Hamaut, A.; Hilbert, H.; Holasppel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Muucelly, M. Cogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Poil, T.M.; Portecelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               extracellular serine
                   A)Cross-references: GB:Z99113, GB:AL009126, NID:g2634090, PIDN:CAB13610.1, PID:e1183385, A)Experimental source: strain 168
C,Genetics:
C,Genetics:
C,Superfamily: subtilisin homology
F;146-398/Domain: subtilisin homology <SBT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microbial serine proteinase (EC 3.4.21.-), minor (vpr), precursor - Bacillus subhicips C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: 17-Jul-1992 #text_change 20-Jun-2000
C; Accession: A41341; Ba1341; S39700, D69730
T; Bacteriol. 173, 6889-6895, 1991
A; Title: Cloning and characterization of the gene for an additional extracellula: A; Reference number: A41341; MUD:92041574; PMID:1938892
A; Title: Cloning and characterization of the gene for an additional extracellula: A; Reference number: A41341; MUD:92041574; PMID:1938892
A; Totle: Cloning and characterization of the gene for an additional extracellula: A; Residues: 1806 < SLO>
A; Residues: 1806 < SLO>
A; Residues: 1600 < SLO>
A; Residues: 161-195 < SLO>
A; Residues: 161-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILSARSSLAPDSSF----WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 WCIQYNEDNPDEPIDIMSMSLGGDALRYDHEQEDPLVRAVEEAWSAGIVVCVAAGNSGPD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQTIASPGVSEKVITVGALDDNNTA----SSDDDTVASFSSRGPTVYGKEKPDILAPGVN 353
                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 DNGHGTHCAGDVASSGASSGQYRGPAPEANLIGVKVLNKQGS-GTLADII-----EGVE
                                                                                                                                                                                                                                                                                                                                                                                                          : | :: | : | | | | | | | | | | EVVRNGQTLTGKGVTVAVVDTGI ----YPHPDLEGRI-----IGFADMVNQKTEPYD
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                                                                                                                                                                                                                                                                                                                                                                  11 DVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNAN-----D
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                          60;
                                                                                                                                                                                                                                                                                                       49; Mismatches 120; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSLLKAALIAGATDIGLGYPSGNQGWGRVTLDKSL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E---VKELLKNGTDKWKDEDPNIYGAGAVNAENSV 439
                                                                                                                                                                                                                                     14.4%; Score 324; DB 2; 31.6%; Pred. No. 2.4e-13;
                                                                                                                                                                                                                                                                                                 Matches 106; Conservative
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A; Residues: 1-806 <GLA>
                                                                                                                                                                                                                                                                          Similarity
Residues: 1-442 <KUN>
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A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seroakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama keuchi, M.; Tamakoshi, A.; Tanamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yata, K.; Yoshikawa, A; Authors: Yoshikawa, H.; Damchin, A.; Ajtitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
A, Accession: D69730
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:299123; GB:AL009126; NID:92636240; PIDN:CAB15835.1; PID:92636344 A;Experimental source: strain 168 C;Comment: The amino terminal sequence of the mature protein and a molecular weight of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
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C;Species: Pyrococcus furiosus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 24-Oct-2000
C;Accession: T28159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---bprgertdhgthyagtvaangti-kgvapdatilayrvlgpgg--sgttenviagve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213;
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C;Superfamily: microbial serine proteinase vpr; subtilisin homology
C;Keywords: hydrolase; serine proteinase
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-160/Domain: propeptide #status predicted <PRO>
F;180-548/Domain: subtilisin homology #status atypical <SBT>
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1larity 23.9%; Pred. No. 1.2e-12;
Conservative 53; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 KNAITVGATE----NLRPSFGSY------
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   Query Match
Best Local Simi
Matches 148;
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R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-799 <STO>
A; Residues: 1-799 <STO>
A; Residues: 1-799 <STO>
A; Residues: 1-799 <STO>
A; Comerical serine proteinase vpr; subtilisin homology
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Ge
R;Voorhorst, W.G.B.; Eggen, R.I.L.; Geerling, A.C.M.; Platteeuw, C.; Siezen, R.J.; Vos, J. Biol. Chem. 271, 20426-20431, 1996
A;Title: Isolation and characterization of the hyperthermostable serine protease, pyroly A;Reference number: 220481; MUID:96355370; PMID:8702780
A;Accession: T28159
A;Accession: T28159
A;Accession: T28159
A;Molecule type: DNA
A;Residues: 1-1398 <-VOo>
A;Residues: 1-1398 <-VOo>
A;Experimental source: DSM3638
C;Generics:
A;Generics:
A;G
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Best Local Similarity 27.9%
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Alkaline serine proteinase (EC 3.4.-.-) I precursor - Alteromonas sp.
NiAlternate names: sutilase
C.Species: Alteromonas sp.
C.Species: Alteromonas sp.
C.Species: Alteromonas sp.
C.Accession: UG4908
B;TSujibo, H.; Myamoto, K.; Tanaka, K.; Kaidzu, Y.; Imada, C.; Okami, Y.; Inamori, X.
Biosci. Blotechnol. Blotechnol.
A;Accession: UG4908
A;Title: Cloning and sequence analysis of a protease-encoding gene from the maxine bact A;Reference number: UG4908; MUID:97141200; PMID:8987544
A;Accession: UG4908
A;Accession: UG4908
A;Status: preliminary
A;Molecule Cype: DNA
A;Residues: 1-715 <TSU-
A;Cross-references: DDBJ:D38600; NID:g1536787; PIDN:BAA18912.1; PID:d1019647; PID:g2160
A;Experimental source: strain O-7
C.Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 450 MLSNEDGLKMRNELENGQNTVTFSIEFDKLVGETVADPSSRGPVMHTWMIKPDVSAPGVA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     678 GYYEGTIIVS------DGSQTVEVPTILFVSEPDYPRVTTFDLDIDENGVLFGSA 726
                                                                                                                                                                                                      218
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVQDGADIMNLSLGNTLNDPDFATSIALDWAMAEGVVAVT-SNGNSGPNNWTVGSPGTSR 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 KPGDFEGVDVEGKIALIVRGEIPFVEKAENAKAAGAVGAIIYNNVAGVQPTVPGLAIPTI 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AALIAGATDI...-GLGYPSGNQG---------WGRVTLDKSLNVAF 320
                                                                                                                                                                                                                                                                            DPNG----HGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTL--FSQ 117
                                                                                                                                                                                                                                                                                                                         ILSARSSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      510 IVSTIPTHQPDDPY-----GYGSRQGTSMASPHVAGAAALLLEAH-PNWGV----DHVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYTGEGITVAILDTGVDYTHPD------LVHAFGDYKGWDFIDNNDDPQETPPG
                                                                                                                                                                                                                                                                                                                                                                                                                     AYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAISVGAT----RLPYNKYKASVFTSDGIDYPSADIMGFPSDEELLELDGETYEYAFAGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VAQFSSRGPT-KDGRIKPDVMAPGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QHFTIHNLSNKRKTYQFDVQFAGNPDGIKVKTSKNLRVQPGKTQ-KINFNVQVDARKLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NGTKYYGNDFTAPYDNNWDGRNNVE---NVFINA---PQSGTYTVEV-------QA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 VNETSSLSTNOKATYSFTAQ-SGKP----LKISLVWSDAPASTSASVTLVNDLDLVITAP
                                                                         244;
                                                                                                                                        GLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGR------TINN-
12.9%; Score 291; DB 2; Length 79 clarity 24.1%; Pred. No. 6.8e-11; Conservative 57; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: aprI
C;Superfamily: subtilisin homology
C;Keywords: hydrolase
F;1-40/Domain: signal sequence #status predicted <SIG>
F;41-150/Domain: amino-terminal propeptide #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAITVGATENLRPSFGSY -----ADNINH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNVPOGPQAFSLAI 432
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the surface lay
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N.Alternate names: hyperthermostable proteinase
C.Species: Staphylothermus marinus
C.Species: Ascession: T29000
R.Mary, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J.
Curr. Biol. 6, 739-749, 1996
A.Title: A hyperthermostable protease of the subtilisin family bound to the surface J.
A.Accession: T29000
A.Mories: 20559; MUID:96385442; PMID:8793300
A.Status: preliminary; translated from GB/EMBL/DDbJ
A.Molecule type: DMA
A.Molecule type: DMA
A.Molecule type: DMA
A.Molecule type: DMS
A.Molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- PVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                ---DVSAPGSSILSTINSGTTTPGS-----ASYASYNGTSMASPHVAGVVALVQS--V 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 APTALTPAAVETLIKNTARALPGAC-----SGGCGAGIVNADAAVTAA-INGGSGGGG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SLSTNOKATYSFTAQSGKPLKISLVWSDAPASTSASVTLV----NDLDLVI---TA 374
      GIPAASSSWHGTHVAGTVAAVTNNTTGVAGTAYGAKVVPVRVLGKCGGSLSDIADAIVWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----LGGLPSNV--STLFSQAYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVL
                                                                                                                                                                                                                                     FAAGNEGPNGGTISAPGTAKNAITVGATEN - - LRPSFGSYADNINHVAQFSSRGPTKDGR
                                                                                                                                                                                                                                                                                                                                                                  IKPDVMAPGTFILSARSS--LAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 KNRGITPK--PSLLK--AALIAGATDIGLGYPSGNQGWGRVTLDKSLNVAFVNETS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 FRGKITALYALGRINNANDPNGHGTHVA-----GSVL----GNGTSNK--GMAPQANLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ARIHINSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNVPQG
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                                                                                                                                                                                                                                                                               VAAGNDASNVSG-SLPANCANVIAVAATTSAGAKASYSNFGTGI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 FQSVMDSNGGLGGLPSNVSTLFSQAYSAG---------
                                                                                                                                                 SGGTVSGIPANANPAEVINMSLGGGGSCSTTMONA-INGAVSRGT-
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C;Species Xanthomonas campestris pv. campestris
C;Date: 21-Nov-1993 #sequence_revision 07-Feb-1997 #text_change 03-Dec-1999
C;Accession: S11890
R;Liu X.N.; Tang, J.L.; Clarke, B.R.; Dow, J.M.; Daniels, M.J.
Mol. Gen. Genet. 220, 433-440, 1990
A;Title: A multipurpose broad host range cloning vector and its use to characterise an e A;Reference number: $11890
A;Accession: S11890
C;Acserimental source: Xanthomonas campestris pv. campestris
A;Note: the sequence from Fig. 4 is inconsistent with that from Fig. 3 in having 205-Ala
C;Superfamily: subtilisin; subtilisin homology
C;Reywords: extracellular protein, hydrolase; serine proteinase
F;1-122/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---DVPAGKTNVTFTMSGGTGDA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNVSTLFSQAYSAGARIHTNSWGAPV-----NGAYTTDSRNVDDYVRKNDMAVLFAAG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VMAPGTFILSARSSLAPDSSFWANHDS-----KYAYMGGTSMATPIVAGNVAQLR-- 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EHFIKN--RGITPKPSLLKAALI--AGATDIGLG----YPSGNQGWGRVTL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPA-STSASVTL---VNDL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSGTVVAVIDTGITSHADLNANILAGYDFISDATTARDGNGRDSNAADEGDWYAANECGA
                                                                                                                                                                                                                                                                                                                                                    GGGVVVAVLDTGYRPHLDLDANILPGYDMISNTFVANDGGARDNDARDPGDAVTRGECGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAAPG----GAQSFADDPEGILSTHNSGSGAPSNDSYHYSQGTSMAAPHVAGVAALIKQA
                                                                                                                                                                                                                                                                                                                                                                                                                                ------NGHGTHVAG---SVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 DSSGQPVPRADQDSSWHGTHVAGTVAAVTNNGEGVAGVAYDAKVVPVRVL---GKCGGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDIADGIIWASGGSDRVPANANPAVVINMSLGGGGACSATTONAINQARNNGTVIVIAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEGPNGGTISAPGTAKNAITVGAT -- ENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPSATPDEVETILKNTTRSFAGSCSNCGTGVVDAAAAVNEALGDVVTPPTGN----TL
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                                                                        <CTP>
F;151-496/Product: alkaline serine protease I #status predicted <MAT>F;182-452/Domain: Bubtilisin homology <SBT:
F;497-715/Domain: carboxyl-terminal propeptide #status predicted <CTP:
F;239-294,335-372,478-481/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130;
                                                                                                                                                                                                                                     136;
                                                                                                                                                                                                                                                                                                21 GQGQVVAVADIG----LDTGRNDSSMHEAFRGKITAIYALGRTNNANDP--
                                                                                                                                                                   12.4%; Score 279; DB 2; Length 715;
.larity 25.9%; Pred. No. 3.4e-10;
Conservative 51; Mismatches 168; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GQGQVVAVADTGL----DTGRNDSSMHEAFRGKITAIYALGRTNNAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.2%; Score 274; DB 2; L. Llarity 27.7%; Pred. No. 5.4e-10; Conservative 53; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ED--GVAKTGLSGAAGSNOFFTF---
                                                                                                                                                                   Query Match
Best Local Similarity
Matches 124; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local Simi
Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              455
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us-09-985-689a-6.rpr

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Subtilisin-type proteinase (EC 3.4.21.-) BH3763 precursor [similarity] - Bacillus halod c) Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Species: Date: 01-Dec-2000 #text_change 15-Jun-2001
C; Accession: C34120
B; Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-4311, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132
A; Accession: C84120
A; Accession: C84120
A; Residues: 1-757 <STO>
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 ANHDSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGYP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 MSLGSSGESSLITNAVN---YSYNKGVLIJAAAGNSGPYQGSIGYPGALVNAVAVAAALEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 GGGINIAVLDIGVNIN-----HPDLRNNVEQCKDFIVGTIYINNSCIDRQGHGIHVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 VL---GNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYSAGARIHTN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 ALADGGTGNGVYGVAPDADLWAYKVLGDDG--SGYADDIAAAIRHAGDQATALNTKVVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 -SWGAPVNGAYTIDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAITVGATEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRPSFGSYADNINHVAQFSSRGPT-KDG----RIKPDVMAPGTFILSARSSLAPDSSFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --FDGGYATISGTSMASPHAAGLAAKIWAQYPSASNVDVRGELQYRAY---ENDILSGYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 VRGMLDEEGVHLTGKGVKVAVIDTGIDYTHPD--LQSSYKGGYDFVDYDDDPMETIASQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RINNANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQGQVVAVADTGLDTGRNDSSMHEAFRGKITAI --YALGRT----NNANDPNGHGTHVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
      A;Cross-references: EMBL:X62369; NID:g40200; PIDN:CAA44227.1; PID:g40201
                              C/Generics:
A/Gene: sub.
A/Gene: sub.
C/Superfamily: subtilisin, bubtilisin homology
C/Superfamily: subtilisin, bydrolase, serine proteinase
C/Superfamily: signal sequence #status predicted <SIG>
F/1-23/Domain: signal sequence #status predicted <PRO>
F/11-2420/Product: microbial serine proteinase #status predicted <PRO>
F/112-420/Product: microbial serine proteinase #status predicted <PRO>
F/145,185,360/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                   26;
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C;Superfamily: microbial serine proteinase vpr; subtilisin homology
C;Keywords: hydrolase; serine proteinase
F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 757;
                                                                                                                                                                                                                                                                                                                                                    Length 420;
                                                                                                                                                                                                                                                                                                                                             12.1%; Score 272; DB 1; Length 42 30.4%; Pred. No. 4.7e-10; ive 41; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.0%; Score 270.5; DB 2; 24.2%; Pred. No. 1.3e-09; iive 48; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SG----NQGWGRVTL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| |:|
AGYGDDFASGFGFATV 419
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.4%
Matches 96; Conservative
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les 127; Conserv
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() Species: Bacillus sp.

() Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jun-1999

() Accession: 823407

R;Narinx, E.; Davail, S.; Feller, G.; Gerday, C.

B;Narinx, E.; Davail, S.; Feller, G.; Gerday, C.

A;Title: Nucleotide and derived amino acid sequence of the subtilisin from the antarctic A;Reference number: 823407; MUD:92256481; PMID:1581352

A;Accession: 823407

A;Residues: 1-420 <NAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S25835
R;Davail, S.; Feller, G.; Narinx, E.; Gerday, C.
Gene 119, 143-144, 1992
A;Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotroph Bacillu A;Reference number: S25835; MUID:93012966; PMID:1398082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                  766
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   ATDIGLGYPSGNOGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWS 352
                                                                                                                                  -DFTAPYDNN 392
                                                                                                                                                                                    DEGPYIGYVLPYLADTDYYGVVKPGSSKNFTLNIVGNGAVSLSAMNTVLYKEYTV~YDGV 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSNK---GMAPQANLVFQSVMDSNGGLGGLFSNVSTLFSQAYSAGARIHTN----SWGA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAITVGATENLRPSF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTY-----RVADFSSRGHKRTAGDYVIQKGDVBISAPGAAVYST-----W--FDG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain TA41)
C.Species: Bacillus sp.
C.Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999
                                                                  --WLAYVSEGIQEAFLENYYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGESSLIT---NAVDYAYDKGVLIIAAAGNSGPKPGSIGYPGALVNAVAALENTIQN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GQGQVVAVADIGLDIGRNDSSMHEAFRGXIIAIYALGRINNANDPNGHGTHVAGSVLGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSYADNINHVAQFSSRGPTKDG-----RIKPDVMAPGTFILSARSSLAPDSSFWANHDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A) Residues: 1-419 < cdav.
A) Residues: 1-419 < cdav.
A) Cross-references: EMBL:X63533; NID:g40198; PIDN:CAA45096.1; PID:g40199
C; Superfamily: subtilish; subtilish; promotogy
C; Keywords: extracellular protein; hydrolase; serine proteinase
F; 1-23/Domain: signal sequence #status predicted <SIG>F; 1-23/Domain: propeptide #status predicted <PRO>F; 1-1419/Product: microbial serine proteinase #status predicted <MAT>F; 111-419/Product: microbial serine proteinase #status predicted <MAT>F; 135-373/Domain: subtilish homology <SBT>F; 144, 184, 359/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
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                                                                                                                                                                                                                                                                                           : | : | : | : | : | XDXSG---LLFLKVPKYAYSGADYVEVVVQLENMTYPPGVF 863
                                                                                                                        DAPASTSASVTLVNDLDLV-ITAPNGTK-----YVGN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.1%; Score 272; DB 1; Luilarity 31.7%; Pred. No. 4.6e-10; Conservative 36; Mismatches 105;
                                           AKDI--WYPAFSQGSGRVDALKAADTVFISE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || : |||||:| || |::
GYATISGTSMASPHAAGLAAKI 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
293
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Search completed: March 31, 2004, 16:10:22 Job time : 13.3508 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q9wtz2 mus musculu	Q9wtz3 rattus norv	Q14703 homo sapien	P11018 bacillus su	P29139 paenibacill	Q9y778 magnaporthe	P41363 bacillus ha	Q09541 caenorhabdi	P16396 bacillus su	Q02470 lactobacill	P20015 tritirachiu	P16271 lactococcus
MS1P MOUSE	MS1P_RAT	MS1P_HUMAN	ISP1_BACSU	ISP PAEPO	SMP1 MAGPO	ELYA_BACHD	YQS6 CAEEL	SUBE_BACSU	P2P LACPA	PRTT TRIAL	PIP LACLC
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                                                                                                                                                                                                                                                                                                                                                                                                             suppressors.";
Proc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).
-!- FUNCTION: Intercellular communication via tagC may mediate integration of cellular differentiation with morphogenesis (By similarity).
-!- SIMILARITY: In the N-terminal section; belongs to peptidase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MDR SUBFAMILY.
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PROSITE; PS50229; ABC_TMLF; 1.

PROSITE; PS50201; ABC_TRANSPORTER_1; 1.

PROSITE; PS50303; ABC_TRANSPORTER_2; 1.

PROSITE; PS00136; SUBTILASE ASP; FALSE_NEG.

PROSITE; PS00136; SUBTILASE_HIS; 1.

PROSITE; PS00138; SUBTILASE_HIS; 1.

PROSITE; PS00138; SUBTILASE_SER; 1.

PROSITE; PS00138; SUBTILASE_SER; 7ALSE_NEG.

Hydrolase; Serine protease; ATP-binding; Transmembrane;
                                                                                                                                                                                                                                                                                                                                    STRAIN=AX4;
MEDLINE=97140317; PubMed=8986798;
Shaulsky G., Escalante R., Loomis W.F.;
"Developmental signal transduction pathways uncovered by genetic
                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Prestalk-specific protein tagC precursor (EC 3.4.21.-).
                                                                                                                                                                                                               Dictyostalium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                PRT; 1743 AA
ALIGNMENTS
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PTR, T18279; T18279.
DictyBase; DDB0001795; tagC.
InterPro; IPR001353; AAA, ATPase.
InterPro; IPR00140; ABC_TM_transpt.
InterPro; IPR00140; ABC_Transporter.
InterPro; IPR000209; Peptidase_SB.
Pfam; PF00065; ABC_Transporter.
Pfam; PF00082; ABC_Trans; 1.
Pfam; PF00082; Peptidase_SB; 1.
PRNTTS; PR00723; SUBTILISIN.
                                                                                                STANDARD;
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Q23868;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                    ----AQSGKPLK---ISLVWSDAPASTSASVTLVNDLDLVITAPNGTKYVGNDFTAPYD 390
565 VESNKLQPTGSLLKALMINNAQLLNGTFQLITSSSITYPSNQVFENFAGASLVQGWGAIR 724
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PROSITE; PS60021; ABC_IMANDORTER_1; 1.
PROSITE; PS60021; ABC_TRANSPORTER_2; 1.
PROSITE; PS600136; SUBTILASE ASP; FALSE_NEG.
PROSITE; PS600137; SUBTILASE HIS; 1.
PROSITE; PS600137; SUBTILASE HIS; 1.
PROSITE; PS600138; SUBTILASE_SER; 1.
Hydrolase; Serine protease; ATP-binding; Transport; Transmembrane; Signal.
                                                                                                                                                                                                                              NGGGSSFLGLAPTQDTLNNVEGIVHNFEPMTYRFMVAGTNVPMGPQNFS 889
                                                                                                                                                                                                      -----NWDGRNNVENVFINAPQSGTYTVEVQAYNVPQGPQAFS 429
                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prestalk-specific protein tagB precursor (BC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
Nol __raxID=44689,
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR00140; ABC_TM_transpt.
InterPro; IPR00140; ABC_TM_transpt.
InterPro; IPR00493; ABC_TMersporter.
InterPro; IPR00649; Peptidase_SB.
Pfam; PP00605; ABC_Transporter.
Pfam; PP00082; Peptidase_SB; I.
Pfam; PR00082; Peptidase_SB; I.
Propom; PR000006; ABC_Transporter; I.
SWART; SW00392; AAA; I.
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                                           312 LDKSLNVAFVNETS--
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                                  PRESTALK-SPECIFIC PROTEIN TAGG. PROTEASE. ABC TRANSPORTER.
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Middle Boulder F., Godsawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Bruschi C.V., Caldwell B., Caldwell B., Carter N.M., Broullet S., Bruschi C.V., Carter N.M., Choi S.K., Codani J.J., Connetton I.F., Cummings N.J., Daniel R.A., Benizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T., Britz C., Fujte M., Golightly E.J., Gralleron N., Ghimsoppi G., Guy B.J., Hage K., Halech J., Harwood C.R., Henaut A., Userler M., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Medique C., Medique C., Medique C., Medidue A., Laylun M., Masuda S., Mauel C., Medique C., Medique C., Medidue R., Luu H., Masuda S., Mauel C., Medique C., Medique C., Medique C., Medique C., Medique C., Mone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parcecan B., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Scholte C., Rocha E., Roche B., Res M., Sadie Y., Sanlan E., Schleich S., Schroeter R., Scoffone F., Schleich G., Schoen B., Schreit H., Takemaru K., Takeuchi W., Tamakoshi A., Taraka T., Terpstra P., Tognoni A., Takeuchi W., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Takeuch W., Wambutt R., Wedler E., Wedler H., Weitzenegger T., A.
                                                                           847 RIVATLVWTDPPSYSGAKFNLVNNLDLLLLNSDDDSIITIGNSGGSLQPAGKVAQP----
                     VKSSNPTPPSRWIGIGGLGKNQKATEWKEDSLSSGLNKSYCFTYKPSSSSSGSGGGGTP
                                                    -LKISLVWSDAPASTSASVTLVNDLDL-----VITAPN--GTKYVGNDFTAPYDNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE=95020537; PubMed=7934828; MEDILINE=95020537; PubMed=7934828; Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W., Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I., Presecan E., Santana M., Schneider E., Schweizer J., Vertes A., Rapoport G., Danchin A.; Rapoport G., Danchin A.; Eaclilus subtlins genome project: cloning and sequencing of the Skb region from 325 degrees to 333 degrees."; Mol. Microbiol. 10:371-384(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sloma A., Rufo G.A. Jr., Theriault K.A., Dwyer M., Wilson S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of the gene for an additional extracellular serine protease of Bacillus subtilis."; J. Bacteriol. 173:6889-6895(1991).
                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Minor extracellular protease vpr precursor (EC 3.4.21.-).
VPR OR IPA-45R OR BSU38090.
Bacillus subtilis.
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                                                                                                                       429
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                                                                                                                                           - DTLNNVEGIIINPTKAMNYKFTIAGTNVPIGPOKFS
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MEDLINE-92041574; Pubmed=1938892;
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MEDLINE=98044033; PubMed=9384377;
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DAGARVHGDSWGSVSLQGYYGGYSDDAGGIDAFLYEYPEFSILRAAGN-NELFASLLAQA
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PRESTALK-SPECIFIC PROTEIN TAGB.
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.ive 72; Mismatches 162; Indels
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                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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REAISVGATQLPLNEYAVTFGSYSSAKVMGYNKEDDVKALNNKEVELVEAGIGEAKDFEG
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GYTGKGIKVAIIDTGVEXNHPDLKKNFGQYKGYDFVDNDYDPKETPTG-------
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., foshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53; Mismatches 155; Indels 213; Gaps
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(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                    Nature 390:249-256(1997)

-: FUNCTION: NOT REQUIRED FOR GROWTH OR SPORULATION.
-: SUBCELLULAR LOCATION: Secreted.
-: PTM: PROBABLY UNDERGOES C-TERMINAL PROCESSING OR PROTEOLYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 318.5; DB 1; Length 806; Pred. No. 5.3e-13;
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    -!- SIMILARITY: Belongs to peptidase family S8.

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Interpro; PRR003137; PA.
Interpro; IPR0030209; Peptidase SB.
Interpro; IPR0090209; Protease_Inhib.
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EMBL, X73124; CAA51601.1; --
EMBL, Z99123; CAB15835.1; --
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HSSP; P00782; 2SBT.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified morprofit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21079021; PubMed=11210516;

Me Vos W.M., Voorhorst W.G.B., Dijkgraaf M., Kluskens L.D.,

de Vos W.M., Voorhorst W.G.B., Dijkgraaf M., Kluskens L.D.,

An der Ocst J., Siezen R.J.;

The "purification, characterization, and molecular modeling of pyrolysin
and other extracellular thermostable serine protesses from
thyperhermophilic micrororganisms.";

Meth. Enzymol. 330:383-393(2001).

-!- FUNCTION: Has endopeptidase activity toward caseins, casein
fragments including alpha-Si-casein and synthetic peptides.

-!- FUNCTION: And pyrolysin seems to be produced by autoproteolytic
activation of HWM pyrolysin.
518 THDPD-----HPYGYGSKQGTSMASPHIAGAVAVIKQ-----AKPKWSVEQIKAAIM 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation and characterization of the hyperthermostable serine procease, pyrolysin, and its gene from the hyperthermophilic archaeon Pyrococcus furiosus.";
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-1- MISCELLANEOUS: Thermostable, high activity at 95 degrees Celsius.
-1- SIMILARITY: Belongs to peptidase family S8.
                                                                              291 AGATDI----GLGYPSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLK
                                                                                                                                                 565 NTAVTLKDSDGEVYPHNAQGAGSARI---MNA--IKADSLVSPGSYSYGTFLKENGNETK
                                                                                                                                                                                                                                        347 ISLVWSDAPASTSASVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDG--RNNVENVFI
                                                                                                                                                                                                                                                                                                               ------NETFILENQ-----SSIRKSYILEYSFNGSGISTSGTSRVVI
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SEQUENCE FROM N.A., SEQUENCE OF 150-184, AND CHARACTERIZATION.
STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
MEDLINE=96355370; PubMed=8702780;
Voorhorst W.G.B., Eggen R.I.L., Geerling A.C.M., Platteeuw C., Siezen R.J., de Vos W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Vol / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.,
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-00T-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Pyrolysin precursor (EC 3.4.21.-).
PLS OR PF0287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1398 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             657 РАНОТСКАТАКУК 669
                                                                                                                                                                                                                                                                                                                                                                                                      405 NAPOSGTYTVEVQ 417
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NCBI_TaxID=2261;
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360 A---SVTLVNDLDLVITAPN----GTKYVGN
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                                                                                                     640 YTELDQGHGLVNVTKSWEI--
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PIR, S11890; S11890.
HSSP; P00782; 2SBT.
MEROPS; S08.UPA; -.
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                                                        Pfam, PF00082; Peptidase_S8; 1.
Pfam, PF04151; PPC; 1.
PRAMTS; PR00723; SUBTILASE_ASP; 1.
PROSITE; PS00136; SUBTILASE_HSS; 1.
PROSITE; PS00139; SUBTILASE_HSS; 1.
PROSITE; PS00139; SUBTILASE_RS; 1.
PROSITE; PS00139; SUBTILASE_RS; 1.
Hydrolase; Serine protease; Glycoprotein; Symogen; Signal;
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355D873A27D56552 CRC64;
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             MEROPS; SOB.100, -.
InterPro; IPR000209; Peptidase_S8
InterPro; IPR007280; PPC.
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REPUBLICE FROM N.A.

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CTRAIN-ATCC 33913 / NCPPB 528;

XX MEDIINE-20202145; PubMed-12024217;

XX da Silva A.C.R.; Ferro J.A.; Reinach F.C.; Farah C.S.; Furlan L.R.;

Alves L.M.C.; do Amaral A.M.; Bertolini M.C.; Camargo L.B.A.;

Alves L.M.C.; do Amaral A.M.; Bertolini M.C.; Camargo L.B.A.;

Ansarotte G.; Cannavan F.; Cardozo J.; Chambergo F.; Ciapina L.P.;

An Cicarelli R.M.B.; Coutlinho L.L.; Cursino-Santos J.R.; El-Dorry H.;

An Faria J.B.; Ferreira A.J.S.; Ferreira R.C.C.; Ferro M.I.T.;

An Faria J.B.; Franco M.C.; Graper A., Lemos B.G.M.; Lemos M.V.F.;

An Cornighieri E.C.; Machadus G.M.; Madeira A.M.B.N.; Martinez-Rossi N.M.;

An Locali E.C.; Machadus M.A.; Madeira A.M.B.N.; Mayaki C.Y.; Moon D.H.;

An Martins B.C.; Machadus G.M.; Menck C.F.M.; Miyaki C.Y.; Moon D.H.;

An Dreira H.A.; Rossi A.; Sena J.A.D.; Silva C.; de Souza R.F.;

A Spinola L.M.; Novo M.T.M.; Okuru V.K.; Oliveira M.C.; Oliveira V.R.;

A Spinola L.M.F.; Tarkita M.A.; Tamura R.B.; Teixeira B.C.; Tezza R.I.D.;

A Setubal J.C.; Kitajima J.F.;

Traindade dos Santos M.; Truiffi D.; Tsai S.M.; White F.F.;

Comparison Of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                  SEQUENCE FROM N.A. MEDINE=90251253; MEDINE=90251253; PubMed=2187155; Liu Y.-N., Tang J.-L., Clarke B.R., Dow J.M., Daniels M.J.; Liu Y.-N., Tang J.-L. Clarke Cloning Vector and its use to characterise an extracellular protease gene of Xanthomonas campestris
246 SKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDI-----GLG
                                                                                                                                                                                   300 YPSGNQGWGRVTLDKSLNVAFVNETSSLSTNOKATYSFTAQSGKPLKISLVWSDAPASTS
                                                                                                                                                                                                                                                                                -----LKAINGTTLPIVDHWADKSYSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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Nature 417:459-463 (2002).
ASTORELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
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01-NOV-1991 (Rel. 20, Last sequence update)
01-REB-2003 (Rel. 41, Last annotation update)
Extracellular protease precursor (EC 3.4.21.-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 IKPDVMAPGTFILSARSS--LAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---DVSAPGSSILSTLNSGTTTPGS-----ASYASYNGTSMASPHVAGVVALVQS--V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GQGQVVAVADIGL----DIGRNDSSMHEAFRGKITAIYALGRINNAND-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSGTVVAVIDTGITSHADLNANILAGYDFISDATTARDGNGRDSNAADEGDWYAANECGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 GIPAASSSWHGTHVAGTVAAVTNNTTGVAGTAYGAKVVPVRVLGKCGGSLSDIADAIVWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 KNRGITPK--PSLLK--AALIAGAIDIGLGYPSGNOGWGRVTLDKSLNVAFVNETS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SLSTNOKATYSFTAQSGKPLKISLVWSDAPASTSASVTLV----NDLDLVI---TA
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SIMILARITY).
SIMILARITY).
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InterPro; IPR007209; Professe_inhib.
InterPro; Prof00920; Protease_inhib.
Pfam; Pr00151; PPC; 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PR00135; SUBTILIASE_ASP; 1.
PROSITE; PS00137; SUBTILIASE_ASP; 1.
PROSITE; PS00138; SUBTILIASE_ESP; 1.
PYGTENTIAL.
SIGNAL
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=29336;
                                                                                                                                                                                                                                     POTENTIAL.
EXTRACELULAR PROTESSE.
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CHARGE RELAY SYSTEM (BY SI
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CHARGE RELAY.
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POTENTIAL.
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01-DBC-1992 (Rel. 24, Created)
01-DBC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Subtilisin precursor (EC 3.4.21.62)
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SEQUENCE FROM N.A.
MEDLINE=92256481; PubMed=1581352;
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Best Local Similarity 27.7
Matches 130; Conservative
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"Nucleotide and derived amino acid sequence of the subtilisin from
the antarctic psychrotroph Bacillus TA39.";
Elochim. Bappys. Accalla:111.13:13.";
Elochim. Bappys. Accalla:111.13:13.";
Elochim. Bappys. Accalla:111.13:13.";

It caralyzes the hydrolysis of proteins and peptide amides.

It caralyzes the hydrolysis of proteins and peptide amides.

In PL Hydrolyzes peptide amides.

In PL Hydrolyzes peptide amides.

In PL Hydrolyzes peptide amides.

In COPACTOR: Binds I calcium ion per subunit (Potential).

In SUBCELLULAR LOCATION: Secreted.

In MISCELLANEOUS: Still active at temperatures close to 0 degrees amize a marked heat lability.

In MISCELLANEOUS: Secretion of subtilisin is associated with onset of sporulation, and many mutations which block sporulation at early stages affect expression levels of subtilisin. However, subtilisin is in not necessary for normal sporulation.

In SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
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PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
Fydrolase; Sporulation; Serine protease; Zymogen; Metal-binding; Calculam-binding; Signal.
SIGNAL 1.26
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 420;
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30.4%; Pred. No. 2.1e-10;
Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR000209, Peptidase S8.
Pfam, PF00082, Peptidase S8, 1.
PRINTS, PR00723, SUBTILISIN.
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HSSP; Q99405; 1MPT.
MEROPS; S08.UPA; -.
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Matches 86; Conserv
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R InterPro; 1PR000209; Peptidase S8.
R InterPro; 1PR00020920; Protease Inhib.
R Ffam; PR00082; Peptidase S8.
R Ffam; PR00082; Peptidase S8;
R PRINTS; PR00123; SUBTILISIN.
R PROSITE; PR00139; SUBTILISIN.
R PROSITE; PR00139; SUBTILISE ASP; 1.
R SIGNAL; 3D-structure.
PROPEP 25 121 THERMOPHILIC SERINE PROTEINASE.
T ACT SITE 193 193 CHARGE RELAY SYSTEM.
T ACT SITE 347 347 CHARGE RELAY SYSTEM.
T METAL 126 CALCIUM 1.
T METAL 126 CALCIUM 3 (VIA CARBONYL OXYGEN).
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95085262; PubMed=7993087;
Maciver B., McHale R.H., Saul D.J., Bergquist P.L.;
"Cloning and sequencing of a serine proteinase gene from a
thermophilic Bacillus species and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALCIUM 1.
CALCIUM 3 (VIA CARBONYL OXYGEN).
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CALCIUM 1.
                                                                                                                          T6-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Thermophilic serine proteinase precursor (EC 3.4.21.-) (Ak.1
                                                                                                                                                                                                    Bacillus sp. (strain AKI).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                   coli.";
Appl. Environ. Microbiol. 60:3981-3988(1994).
                                                                                                     401 AA
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   SG----NQGWGRVTL 312
                             404 AGYGDDFASGFGFATV 419
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41100272301112
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PDB; IDBI; 18-NOV-99.
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045670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 HGTHVAG----SVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYSAGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IHTINSWGAPVNGAYTIDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNALIVGA
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CALCIUM 3.
CALCIUM 1.
CALCIUM 1 (VIA CARBONYL OXYGEN).
CALCIUM 1 (VIA CARBONYL OXYGEN).
SODIUM (VIA CARBONYL OXYGEN).
SODIUM (VIA CARBONYL OXYGEN).
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ilarity 32.6%; Pred. No. 5.9e-10;
Conservative 28; Mismatches 95;
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TENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWANH 244
                                                                                                                                                                                               STRAIN=YII;
MEDLINE=90216674; PubMed=2182621;
MEDLINE=90216674; PubMed=2182621;
Thrada I.; Kwon S.-T., Miyata Y., Matsuzawa H., Ohta T.;
"Unique precursor structure of an extracellular protease, aqualysin "Unique precursor structure of an extracellular protease, aqualysin I, with NH2- and COOH-terminal pro-sequences and its processing in Escherichia coli.";
Bacherichia coli.";
J. Biol. Chem. 265:6576-6581(1990).
                                                                                                                                                                                                                                                                                       Kwon S.-T., Terada I., Matsuzawa H., Ohta T.,
"Nucleotide sequence of the gene for aqualysin I (a thermophilic
alkaline serine protease) of Thermus aquaticus YT-1 and
characteristics of the deduced primary structure of the enzyme.";
Eur. J. Biochem. 173:491-497(1988).
                                                                                                                                                        Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
               ----vòqydrlásfsnygtw-----vovvápgvolvstitg---
                                                                                                                                                                                                                                                                 SEQUENCE OF 75-442 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                       01-AUG-1988 (Rel. 08, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-BPEB-2003 (Rel. 41, Last annotation update)
Aqualysin I precursor (EC 3.4.21.-).
                                                                                         513 AA
                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 15-23.
                                         338 -NRYAYMSGTSMASPHVAGLAALL 360
                               DSKYAYMGGTSMATPIVAGNVAQL 268
                                                                                                                                                                                                                                                                                MEDLINE=88225062; PubMed=3286255;
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                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T.-ENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWA 242
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                                                                                                                                                                                                                                                                                                                                                                                    16 SYGLYGOGOWYAVADTGLDTGRNDSSMHEAFRGKITAIY-ALGRINNANDPNGHGTHVAG
                                                                                                                                                                                                                                                                                                                                                                                                                     152 TYTATGRGVNVYVIDTGIRT-----THREFGGRARVGYDALG--GNGQDCNGHGTHVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 SVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYSAGARIHTNSWGAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 ----VNGAYTIDSRNVDDYVRKNDMAV----LFAAGNEGPNGGTISAPGIAKNAITVGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 LGYP-----SGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 SGSPNRLLYSLLSSGSGSTAPCTSCSYYTGSLSGPGDYNFQPNGTYYYS-----PAGTHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 VWSDAPASTSASVTLVNDLDLVITAPNGTKY--VGNDFTAPYDNNWDGRNNVENVFINAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P54423; 006726; 01-200-1996 (Rel. 34, Created) 15-DEC-1998 (Rel. 34, Last sequence update) 16-DEC-1998 (Rel. 37, Last sequence update) 10-OCT--2003 (Rel. 42, Last annotation update) Cell wall-associated procease precursor (EC 3.4.21.-) [Contains: Cell wall-associated polypeptides CWBP23 and CWBP52].
                                                                                                                                                                                                                     (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                              ; Pred. No. 1.5e-09; 43; Mismatches 157; Indels 111;
                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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CHARGE RELAY SYSTEM (BY SI
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DDFDFE6D4A50B785 CRC64;
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STRAIN=168;
MEDLINE=97158234; PubMed=9004506;
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InterPro; IPR000209; Peptidase S8.
InterPro; IPR09020; Protease Inhib.
Pfam, PR00020; Peptidase S8; I.
PRINTS; PR00723; SUBTILISIN.
PROSTE; PS00136; SUBTILISIN.
PROSTE; PS00136; SUBTILASE ASP; I.
PROSTE; PS00137; SUBTILASE SER; I.
Hydrolase; Serine protease; Zymogen; Signal.
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127
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513 AA;
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Best Local Similarity
Matches 122; Conserv
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Bacillus subtilis
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REC MEDIINE-98044033; PubMed-9384377;

REC MEDIINE-98044033; PubMed-9384377;

REC AZEVEDOUGE TO GORGAMAN M. MOSZET I., ROLOCHIN A., Borchert S., AZEVEDOU V., BELTETO M.G., BESSIERS P., BOLOCHIN A., BORCHET S., BLUECHI C.V., Caldwell B., Capuano V., Carter N.M., ALOCANI J.C., CONNECTON I.F., Cummings N.J., Daniel R.A., RA Entian K.D., Erington J. Fabre C., Ferrari E., Foulger D., RA Entian K.D., Erington J., Fabre C., Ferrari E., Grandi G., Gulszp. P., Goffeau A., Golightly E.J., Grandi G., Guls B.J., Haga K., Haiech J., Harwood C.R., Henaut A., A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., A., Gulseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., A., Gulseppi G., Guy B.J., Haga K., Haiech J., Mannel C., Medigue C., Rorita K., Lapidus A., Lardinois S., Hauber J., Lazarevic V., R.A. Kusta K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., R.A. Medina N., Mellado R.P., Liu H., Masuda S., Mauel C., Medigue C., Media N., Mellado R.P., Miruh M., Mostel D., Portetelle D., Portetelle D., Portetelle D., Portetelle D., Rose M., Sadaie Y., R.A. Presecan E., Bujic P., Purnelle B., Rapoport G., Rey M., Scallan E., Schleich S., Schroeter R., Scoffene F., Sekiguchi J., Sekowska A., Seros S.J., Serror P., Shin B.S., Soldo B., Rateuchi M., Tamakoshi A., Tanaka T., Terpstra P., Takamatu K., Tanaka T., Terpstra P., Takamatu K., A. Tanaka T., Terpstra P., Tognoni A., Tasarot N., Wallers P., Wipat R., Wander E., Wedler E., Woolki K., Yoshikawa H.F., Zumstein B., Yoshikawa H.P., Zumstein B., Yoshikawa H., Danchin A., Nahuri S., Solochin S., Schroeter R., Schiladon S., Wallers P., Wipat S., Schiladon S., Wallers P., Wipat S., Wallers P., Wipat S., Wallers P., Wipat S., Schiladon S., Wallers P., Wipat S., Schiladon S., Wallers P., Wallers P., Wallers P., Wallers P., Wallers P., Schiladon
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he wprA gene of Bacillus subtilis 168, expressed during exponential cowth, encodes a cell-wall-associated protease."; crobiology 142:3437-3444 (1996).
                                                                                                                                    Seror S.J.;
and citG (289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: NOT YET KNOWN; COULD BE INVOLVED IN PROTEOGLYCAN DEGRADATION, BY CLEAVAGE OF ITS PEPTIDE BRIDGES.
-!- SUBCELLULAR LOCATION: Cell-wall bound.
-!- PTM: PROCESSED INTO CWBP23 AND CWBP52.
-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                  Medina N., Vannier F., Roche B., Autret S., Levine A., "Sequencing of regions downstream of adda (98 degrees) degrees) in Bacillus subtilis."; Microbiology 143:3305-3308(1997).
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InterPro; IPRO00209; Peptidase_S8.
PETam; PRO0082; Peptidase_S8; 1.
PRO723; SUBTILISIN.
PROSTIE; PSO0136; SUBTILASE_ASP; FALSE_NEG.
PROSTIE; PSO0137; SUBTILASE_HIS; 1.
PROSTIE; PSO0137; SUBTILASE_HIS; 1.
                                                                                                              MEDLINE=98015415; PubMed=9353931;
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                                                                              SEQUENCE FROM N.A.
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139 TIDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAITVGATENLRPSFGSYADN 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 TYSFTAQSGKPLKISLVW-----SDAPASTSASVTLVNDLDLVITAPNGTKYVG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GWGRVTLDKSLNVA----FVNETSSLST-------NQKA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               767 LGSAKAGKUNAFKVNIATQKQDQVLYLKATKGDAKTSYKVVVVKG-----KPSGTPKVN 820
                                                                                                                                                                                                                                                                                                                                                                                                                                    LIAVVDTGVDSTLAD-----LKGKVRTDLGHNFVGRNNNAMDDQGHGTHVAGIIAAQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYSAGARIHTNSWGAPVNGAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       654 PYAAAAGLL---FAQNPKLKRTEVEDMLKKT----ADDISFESVDGGEEELYDDYGDPI
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                                                                                                                                                  (BY SIMILARITY). (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                61, Mismatches 157; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       821 AVKTK--DTAVKGKANSKAMIRVKNKSKKVIASAKADAKGTFSVKIK 865
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                                                                 WALL-ASSOCIATED PROTEASE.
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01-APR-1993 (Rel. 25, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Subtilisin Savinase (BC 3.4.21.62) (Alkaline protease).
Bacillus lentus.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
protease; Cell wall; Zymogen; Signal;
                                                                                                                                                                                                                                                             OF67C353E55F8DBC CRC64;
                                                                                                                                                CHARGE RELAY SYSTEM
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                                                                                                                                                                                                                                                                                                       11.5%; Score 259; DB 1;
ilarity 25.1%; Pred. No. 3.8e-09;
Conservative 61; Mismatches 157,
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L -> I (IN REF. 1)
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Betzel C., Klupsch S., Papendorf G., Hastrup
Wilson K.S.;
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MEDLINE=96184541; PubMed=8654411;
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96487 MW;
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"Backbone dynamics of the 269-residue p
from 15N-NMR relaxation measurements";
Eur. J. Biochem. 235:629-640(1996).
                                                                                                                                       X-RAY CRYSTALLOGRAPHY (0.78 ANGSTROMS).
MEDLINE=98426039; PubMed=9753430;
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                                                                                                                                                                                                                                                                                                                                                                                                           243
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                                                                                                                                                                                                           11 VOAPAAHNR-GLTGSGVKVAVLDTGIST-----HPDLNIRGGASFVPGEP-STQDGNG
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                                                                                                                                                                                                                                                                                                 62 HGTHVAGTIAALNNSIGVLGVAPSAELYAVKVLGASG--SGSVSSIAQGLEWAGNNGMHV
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"Cloning, characterization, and multiple chromosomal integration of a Bacillus alkaline protease gene.";
Appl. Environ. Microbiol. 57:901-909(1991).
                                                                                                                                                          8 VKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNG
                                                                                                       54; Gaps
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STRAINEPB92,
MEDLINE-91282483; PubMed=2059048;
van der Laan J.C., Gerritse G., Mulleners L.J.M., van der Hoek R.A.,
                                                   Length 269;
                                                   11.4%; Score 257; DB 1; Length 26 30.3%; Pred. No. 1.1e-09; ive 38; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1445;
  26698 MW; 4D89F8778999BF8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Rataline protease precursor (EC 3.4.21..).
                                                Query Match
Best Local Similarity 30.3%;
Matches 91, Conservative
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269 AA;
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P27693;
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--STYASLNGTSMATPHVAGAAALVKQKNPSWSNVQIRNHLKNTATSLGSTNL---YGSG 371
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STRAIN=221 / ATCC 21522 / JCM 9139 / DSM 2512;
STRAIN=210 / ATCC 21522 / JCM 9139 / DSM 2512;
STRAIN=91043753; PubMed=1368952;
Takami H., Kobbayashi T., Kobayashi M., Yamamoto M., Nakamura S., Aono R., Horikoshi K.;
Molecular cloring, nucleotide sequence, and expression of the "Molecular cloring, nucleotide sequence, and expression of the structural gene for alkaline serine protease from alkaliphilic Bacillus sp. 221.";
Biosci. Biotechnol. Biochem. 56:1455-1460(1992).
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11.4%; Score 257; DB 1; Length 38
Best Local Similarity 30.3%; Pred. No. 1.7e-09;
Matches 91; Conservative 38; Mismatches 117; Indels
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AC P41362,

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 42, Last annotation update)

DT Alkaline protease precursor (EC 3.4.21.-).

DS Bacillus clausii.

OC Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TAXID=79880;
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MEDLINE=97277237; PubMed=9115441;
Martin J.R., Mulder F.A., Karimi-Nejad Y., van der Zwan J.,
Martini M., Schipper D., Boelens R.;
"The solution structure of serine protease PB92 from Bacillus
alcalophilus presents a rigid fold with a flexible substrate-binding
                                                                                                                           MEDLINE=92390330; PubMed=1518788; van der Laan J.C., Teplyakov A.V., Kelders H., Kalk K.H., Misset O., Mulleners L.J.M., Dijkstra B.W.; "Crystal structure of the high-alkaline serine protease PB92 from Pacillus alcalophilus."; Protein Eng. 5:405-411(1992).
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MEDLINE=30708250; Pubmed=1447775;
Sobek H., Hecht H.-J., Achle W., Schemburg D.;
"X-ray structure determination and comparison of two crystal a variant (RanliSarg) of the alkaline protease from Bacillus alcalophilus refined at 1.85-A resolution.";
J. Mol. Biol. 228:108-117(1992).
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-!- COFACTOR: Binds 2 calcium ions per subunit.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to peptidase family S8.
                                               CRYSTALLOGRAPHY (1.75 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M65086; AAA2212.1; -.. EMBL; A13738; CAA01128.1; -. PIR; A49778. PBDB; 1AH2; 15-APR-98. MEROPS; SOB.038; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 112-380.
                                                                                               STRAIN=PB92;
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186 B--NLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWAN 243
                                                                 -----DIVAPGVNVQSTYPG-----
                                                                                                                           244 HDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGYPSG
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MEDLINE=95358832; PubMed=7632397;
Kobayasahi T., Hakamada Y., Adachi S., Hitomi J., Yoshimatsu T.,
Koke K., Kawai S., Ito S.,
Purification and properties of an alkaline protease from
alkalophilic Bacillus Sp. KSM-KK6.";
Appl. Microbiol. Biotechnol. 43:473-481(1995).
-!- COPACTOR: Binds Z calcium ions per subunit.
-!- SUBUNIT: Monomer.
-!- SINILARITY: Belongs to peptidase family S8.
PDB; IMPT, 22-UVM-94.
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Yamane T., Kani T., Hatanaka T., Suzuki A., Ashida T.,
Kobayashi T., Ito S., Yamashita O.;
"Structure of a new alkaline serine protease (M-protease) from
Bacillus sp. KSM-KI6.";
Acta Crystallogr. D 51:199-206(1995).
                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
M-protease (EC 3.4.21.-)
Bacillus sp. (strain KSM-K16).
Bacteria; Firmicutes; Bacillales; Bacillus.
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                                                                       286 DONNNRASFSOYGAGL-----
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099405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS, 208.103.
InterPro; IPR000209; Peptidase S8.
InterPro; IPR000209; Peptidase S8.
InterPro; Pr000820; Peptidase S8; I.
PRONOS2; Peptidase S8; I.
PROSITE; PS00134; SUBTILASE ASP; I.
PROSITE; PS00135; SUBTILASE_HIS; I.
PROSITE; PS00138; SUBTILASE_ER; I.
Hydrolase; Serine protease; Zymogen; Metal-binding; Calcium-binding;
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHACUM 1 (BY SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM 2 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
                                                                                                                                                                                                      Weinheim (1991).
--- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
--- SUBCELLUIAR LOCATION: Secreted.
--- SIMILARITY: Belongs to peptidase family S8.
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11.4%; Score 257; DB 1; Length 380;
Best Local Similarity 30.3%; Pred. No. 1.7e-09;
Matches 91; Conservative 38; Mismatches 117; Indels
                                                                                                                                     (In) Horikoshi K. (eds.);
Microorganisms in alkaline evironments, pp.187-194, VCH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5F73ABC68D5B6831 CRC64;
                POTENTIAL.
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EMBL, D13157; BAA02442.1; -..
EMBL, A26817, CAA01836.1; -..
EMBL, A22550; CAA01611.1; -..
HSSP, P29600; 1GCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 RGKITAIY-ALGRINNANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVM--DSNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVMAPGIFILSARSSLAPDSSFWANHDSKYAYMGGISMATPIVAGNVAQLREHFIKNRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVFAPGSQIKSA-------YDGGYKTISGTSMATPHVAG-VAAL--YLQENSSV
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                                                                    calcium-dependent,
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[1]

SEQUENCE FROM N.A. Mode=2546861; Mode D.R.; Deane S.M., Robb F.T., Robb S.M., Woods D.R.; Moclectide sequence of the Vibrio alginolyticus caldetergent-resistant alkaline serine exoprotease A."; Gene 76:281-288(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.2%; Score 252.5; DB 1;
llarity 26.1%; Pred. No. 5e-09;
Conservative 61; Mismatches 151;
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CHARGE RELAY SYSTEM
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PRINTS; PR00723; SUBTILASE ASP; 1.
PROSITE; PS00136; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
PROPER 1.2
PROPER 2. 141
PROPER 2. 141
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PATRALINE SERINE
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PIR, JS0173, JS0173.
HSSP, Q99405, 1MPT.
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Vibrio alginolyticus.
Vibrio alginolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=663;
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28-FEB-2003 (Rel. 41, Last annotation update)
Alkaline serine exoprotease A precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%; Score 255; DB 1;
30.4%; Pred. No. 1.4e-09;
iive 32; Mismatches 102
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01-AUG-1990 (Rel. 15,
28-FEB-2003 (Rel. 41,
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269 AA;
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Best Local Similarity
Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRANT-NCIB 6816;
MEDLINE-8609368; PubMed=3001653;
Jacobs M., Eliasson M., Uhlen M., Flock J.-I.;
"Cloning, sequencing and expression of subtilisin Carlsberg from Bacillus licheniformis.";
Nucleic Acids Res. 13:8913-8926 (1985).
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MEDLINE=68234702; PubMed=4967581;
Smith E.L., Delange R.J., Evans W.H., Landon M., Markland F.S.;
Smith E.L., Delange R.J., The complete sequence; comparison with
"Subtilisin Carlsberg. V. The complete sequence; comparison with
subtilisin BFN'; evolutionary relationships.";
J. Blol. Chem. 243:2184-2191(1968).
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MEDLINE=33291170; PubMed=8512925;
Syed R., Wu Z.P., Hoggle J.M., Hilvert D.;
ECrystal structure of selenosubtilisin at 2.0-A resolution.";
Biochemistry 32:6157-6164(1993).
485 AK------PTLNAWDCRPFKYGNNETCTVSATQSGRYHVMIQGYS 523
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Bacillus licheniformis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1402;
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                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-CCT-2003 (Rel. 42, Last annotation update)
Subtilisin Carlsberg precursor (EC 3.4.21.62)
                                                                                                                                     379 AA
                                                                                                                                        PRT;
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                                                                                                                                        STANDARD;
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PDB; 1AF4; 16-JUN-97.
PDB; 1AV7; 01-APR-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 ---STYATLNGTSMASPHVAGAAALI------LSKHPNLSASQVRNRLSSTATYLGS 363
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                                                                                                                                                                                                                                                                                                                                                                    7 IVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTNNANDPN 66
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                  59;
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38908 MW; F19A6DC5761FB504 CRC64;
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Best Local Similarity 30.2%
Matches 92; Conservative
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379 AA;
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364 SFYYG 368
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Search completed: March 31, 2004, 16:05:32 Job time: 8.51154 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	US-09-985-689A-7 US-09-985-689A-1	US-10-385-662-2 US-09-985-689A-2	US-09-985-689A-6 US-09-985-689A-5	US-09-985-689A-3 US-09-985-689A-4	US-10-336-324-10	US-10-403-105-13 US-10-090-624-12	US-10-090-624-1	US-10-090-624-4 US-10-090-624-16	US-10-156-761-13251
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1079	1139	1237	1398	519	19725	580	418	595	1101	368	663	271	627	271	271	271	271	271	271	271	271	271	269	269	269	269	269	269	269
15.2	14.7	14.3	13.6	13.2	13.2	12.4	12.1	12.1	11.5	11.5	11.3	11.2	11.2	11.2	11.1	11.1	11.1	11.1	11.1	11.1	11.0	11.0	10.9	10.9	10.9	10.9	10.9	10.9	10.9
341.5	332	323	306	297	297	279.5	271.5	271.5	259.5	258	253.5	252.5	252	251.5	Ψ.			249.5	249.5	249.5	247.5	247.5	'n	245.5	ம	10	245.5	245.5	245.5
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	4	41	42	4.	44	45

## ALIGNMENTS

RESULT 1

																										DB 10; Length 433;	40-107;	ss 0; Indels 0; Gaps .	SLDTGRNDSSMHEAFRGKITALYALGRIN	3LDTGRNDSSMHEAFRGKITALYALGRTN	/FQSIMDSGGGLGGLPANLQTLFSQAYSA
7	Sequence 7, Application US/09985689A Publication No. US2003002351A1	RMATION:	HATADA, YUJI	OGAWA, AKINORI		SATO, TSUYOSHI	ARAKI, HIROYUKI					INCE: 215483US0	APPLICATION NUMBER: US/09/985,689A	CORRENT FILLING DATE: ZOUZ-U/-UI	APPLICATION NUMBER: JP P2000-355166	FILING DATE: 2000-11-22	PRIOR APPLICATION NUMBER: JP P2001-114048	PRIOR FILING DATE: 2001-04-12	SEQ ID NOS: 7	PatentIn version 3.1		33		ORGANISM: Bacillus sp.	7-7	100.0%; Score 2252	100.0%;	vative 0;	NDVARGIVKADVAQNNFGLYGQQQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRT	NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN	NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA
US-09-985-689A-7	Sequence 7,	GENERAL INFORMATION:	; APPLICANT:	; APPLICANT:	; APPLICANT:	; APPLICANT:	; APPLICANT:	; APPLICANT:	, APPLICANT:	, APPLICANT:	, TITLE OF II		CURRENT API	; CORRENT FIL		, PRIOR FILLI	, PRIOR APPL.	, PRIOR FILLI	; NUMBER OF (	SOFTWARE: 1	; SEQ ID NO 7	; LENGTH: 433	; TYPE: PRT	, ORGANISM:	US-09-985-689A-7	Query Match	Best Local Similarity	Matches 43	Qy 1	1 qq	Oy 61

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61 NANDPNGHGTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 119
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                           241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITFKPSLLKAALIAGAADIGLGY
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TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
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94.4%; Score 2125.5; DB 1:
Best Local Similarity 93.5%; Pred. No. 3.3e-178;
Matches. 406; Conservative 19; Mismatches 8;
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APPLICANT: SATO, TGTYOSHI

APPLICANT: SATO, TGTYOSHI

APPLICANT: SATO, TGTYOSHI

APPLICANT: SATO, KAZUHINO

APPLICANT: IZANA, YOSHIFUMI

APPLICANT: IZANA, YOSHIFUMI

APPLICANT: ROBAYASHI, TOHNU

APPLICANT: NOWTZA, MASAFUMI

TITLE OF INVENTION: Alkaline protease

TILE REPERENCE: 234938160

CURRENT FILING DATE: 2003-03-12

CURRENT APPLICATION NUMBER: UP 2002-165987

PRIOR PELING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: UP 2002-165987

PRIOR PELING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: UP 2002-304230

PRIOR PLING DATE: 2002-10-18

PRIOR PLING DATE: 2002-10-18

PRIOR PLING DATE: 2002-10-18

PRIOR FILING DATE: 2002-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/10385662; Publication No. US20040002432A1; GENERAL INFORMATION:
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US-10-385-662-2
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                        NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA
                                                                            GARIHTINSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGFGSGTISAFGTAKNAIT
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94.4%; Score 2125.5; DB 10; Lengt
Best Local Similarity 93.5%; Pred. No. 3.3e-178;
Matches 406; Conservative 19; Mismatches 8; Indels
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APPLICANT: GGAMA, AKINGRI
APPLICANT: GGAMA, AKINGRI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: SUNTTOWN, NOBUTUKI
APPLICANT: SAEXI, KATSUHISA
TITLE REPRENUE: 215483150
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR FILING DATE: 2001-011-22
PRIOR FILING DATE: 2001-011-22
PRIOR FILING DATE: 2001-04-12
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US-09-985-689A-1
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301 PNGNQGWGRVTLDKSLNVAYVNESSALSTSQKATYTFTATAGKPLKISLVWSDAPASTTA 360
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                                                                                   361 SVTLVNDLDLVITAPNGTRYVGNDFSAPFDNNWDGRNNVENVFINSPQSGTYTIEVQAYN
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                                                           SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
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                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09985689A
Publication NO. US20030022351A1
GENERAL INFORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: GOAWA, AKINORI
APPLICANT: SAGEYAMA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SUMITOWO, NGBUYUKI
APPLICANT: SUMITOWO, NGBUYUKI
APPLICANT: SAEXI, HIROYUKI
APPLICANT: SAEXI, KATSUHISA
ITILE OF INVENTION: Alkaline proteases
FILE REFERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SEQ ID NOS: 7
SEQ ID NOS: 7
SEQ ID NOS: 7
SEQ ID NOS: 7
SED ID NOS: 7
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                                                                                                                                                                   420 VPVSPOTFSLAIVH 433
                                                                                                                                                                                                    ORGANISM: Bacillus sp. US-09-985-689A-6
                                                                                                                                                                                                                                                                                                                                          -09-985-689A-6
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                                                                 241 WANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY
                                                                                                                                                                            301 PNGNQGWGRVTLDKSLNVAYYNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA
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                                                                                                                                           PNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA
                                                                                                                                                                                                                                                    SLILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
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Best Local Similarity 93.3%; Pred. No. 1.3e-177;
Matches 405; Conservative 18; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Publication US/09985689A
Publication No. US20030022351A1
GENERAL INFORMATION:
APPLICANT: HATADA, YUUI
APPLICANT: GGMAA, AKINORI
APPLICANT: GGMAA, AKINORI
APPLICANT: RAGEYAMA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SUMITOMO NOGUYUKI
APPLICANT: SARKI, KATSUHISA
ILIE OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
ILIE OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
ILIE REPERRUCE: 215483USO
CURRENT FILING DATE: 2002-07-01
PRIOR FILING DATE: 2000-11.22
PRIOR FILING DATE: 2000-11.22
NUMBER OF SEQ ID NOS: 7
SEQ ID NOS: 7
SEQ ID NOS: 7
SEQ ID NOS: 7
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ORGANISM: Bacillus sp.
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361 YILVNDLDLVITAPNGQKYVGNDFSYPYDNNMDGRNNVENVFINAPQSGTYTIEVQAXNV 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.6%; Score 2040; DB 10;
88.9%; Pred. No. 1.1e-170;
iive 24; Mismatches 24;
                                                    APPLICANT: HATADA, YUJI
APPLICANT: OGAWA, AKINORI
APPLICANT: OGAWA, AKINORI
APPLICANT: SATO, TSUSOSHI
APPLICANT: SATO, TSUSOSHI
APPLICANT: APARI, HIROVUKI
APPLICANT: SUMITOWO, NOBUVKI
APPLICANT: SUMITOWO, NOBUVKI
APPLICANT: SUMITOWO, MITSUYOSHI
APPLICANT: SISHI, KATSUHISA
TILE REFERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2000-01-02
PRIOR APPLICATION NUMBER: UP P2000-355166
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 7
SEQ ID NOS: 7
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Publication No. US20030022351A1
GENERAL INPORMATION:
A PPLICANT: HATADA, YUJI
A PPLICANT: OGAWA, AKINORI
A PPLICANT: SATO, TSUYOSHI
A PPLICANT: SATO, TSUYOSHI
A PPLICANT: ARAEXAMA, YASOSHI
A PPLICANT: ARAEXI, HIROYUKI
No. US20030022351A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.9%
Matches 385; Conservative
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Best Local Similarity 89.1%; Pred. No. 4.8e-171;
Matches 386; Conservative 24; Mismatches 23;
                                                                                                                                                                                       CS-09-985-689A-5-98-9-5-9-5-98-985-689A
PUBLICALION NO. US20030022351A1
GENERAL INFORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: AGGRAA, AZINORI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SAEXI, KATSUHISA
ITILE ON INVENTION: ANISUYOSHI
APPLICANT: SUMITOMO, NOBUYUI
APPLICANT: SAEXI, KATSUHISA
ITILE ON INVENTION: AIRAILINE
FILE REFERENCE: 215483USO
CURRENT APPLICATION NUMBER: US P2000-355166
PRIOR FILING DATE: 2002-07-01
PRIOR FILING DATE: 2001-04-12
NUMBER: OF SEQ ID NOS: 7
SEQ ID NO S: 7
SEQ ID NO SEX ID NO S
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US-09-985-689A-3
; Sequence 3, Application US/09985689A
|| || || || || || || || || || || || 421 VPQGPQAFSLAIVN 434
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ORGANISM: Bacillus sp
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APPLICANT: Hansen, Peter K.
APPLICANT: Hansen, Peter K.
APPLICANT: Hansen, Peter K.
APPLICANT: Hansen, Peter K.
APPLICANT: Mikkelsen, Frank
ITLE OF INVENTION: Protease Variants And Compositions
FILE REFERENCE: 5435.200-US
CURRENT APPLICATION WUMBER: US/10/403,105
CURRENT APPLICATION WUMBER: US/09/196,281A
PRIOR PILING DATE: 203-03-03-31
PRIOR PILING DATE: 1998-11-19
PRIOR PILING DATE: 1998-11-19
PRIOR PILING DATE: BALLER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 345
ITTRE: PRIOR P
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                                                                                                                                                                                                                        Query Match 73.2%; Score 1649; DB 14; Best Local Similarity 100.0%; Pred. No. 1.9e-136; Matches 317; Conservative 0; Mismatches 0;
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           SEQ ID NO 10
LENGTH: 345
TYPE: PRT
ORGANISM: Bacillus
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Publication No. US20030176304A1
GENERAL INFORMATION:
APPLICANT: Hansen, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelsen, Frank
APPLICANT: Mikkelsen, Frank
APPLICANT: Mikkelsen, Frank
TITLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5349.204-US
FURRENT APPLICATION NUMBER: US/10/336,324
CURRENT FILING DATE: 2003-01-03
FRIOR PLILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 88.7%; Pred. No. 4.4e-170;
Matches 384; Conservative 25; Mismatches 24;
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
ITILE OF INVENTION: Alkaline proteases
FILE REFERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: JP P2000-355166
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2010-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 4
LENGTH: 433
TYPE: PRI
TYPE: PRI
TYPE: PRI
CSCANISM: Bacillus SP.
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US-10-336-324-10
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243 HDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPK--PSLLKAALIAGA----- 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 WDNAN------SDLDLYLYDPNGNQ-VDYSYTAYY------GFEKVGYYNPTDG 381
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                                                                                                                                                                                                                                                                                                   APPLICANT: TAYCAKURA, Hikaru
APPLICANT: MARAKURA, Michael
APPLICANT: MORISHITA, Michael
APPLICANT: MORISHITA, Michael
APPLICANT: MATO, Ivancko
APPLICANT: KATO, Ivancko
APPLICANT: KATO, Ivancehin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAURAE
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DATE: 1099-10-06
PRIOR FILING DATE: 1999-10-06
PRIOR PILING DATE: 1999-10-06
PRIOR PILING DATE: 1999-10-06
PRIOR PILING DATE: 1997-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.6%; Score 396; DB 13; Length 4 29.5%; Pred. No. 3.7e-26; cive 56; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10090624
Publication No. US20020132335A1
GENERAL INFORMATION:
                                                                                                                                                                                                                   Sequence 1, Application US/10090624 Publication No. US20020132335A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Pyrococcus furiosus
US-10-090-624-1
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| SOG GYYNPTAGTWTVKVVSY
402 FINAPOSGTYTVEVQAY
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127; Conservative
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US-10-090-624-4
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Best Local S:
Matches 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLVWSDAPGSTTASLTLV----NDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENV 401
                                                                                                                                                                                                                                                  269 ANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHGTHVAGSVLG----NATNKGMAPQANLVFQSIM--DSGGGLGGLPANLQTLFSQAYSA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GARIHINSWGAPVNGAYTIDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 ANHDSKYAYMGGTSMATPIVAG-NVAQLREHFVKNRGVTPK--PSLLKAALIAGA---- 292
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149 GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT 208
                                                                                                         209 VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW 268
                                                                                                                                                                                                 241 ANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USERIAL TARGET OF APPLICATION US/10090624

PUBLICATION NO. US20020132335A1

GENERAL INFORMATION:

APPLICANT: TAKAKURA, Hikaru

APPLICANT: TAKAKURA, Hikaru

APPLICANT: MORISHITA, Mio

APPLICANT: MORISHITA, Mio

APPLICANT: MAJOA, TAMOKO

APPLICANT: KATO, IKUNOSHIN

TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

CURRENT APPLICATION NUMBER: US/10/090,624

CURRENT APPLICATION NUMBER: US/10/090,624

CURRENT APPLICATION NUMBER: 1590-464

PRIOR APPLICATION NUMBER: 1599-445,472

PRIOR APPLICATION NUMBER: 1599-410

PRIOR PRIING DATE: 1997-06-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PALENTIN VERSION 3.0

SEQ ID NO 12

LENGTH: 659

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                                                                                                                                                                                                                                                                                                                                NGNOGWGRVTLDKSLNV 317
                                                                                                                                                                                                                                                                                                                                                                                           329 NGNOGWGRVTLDKSLNV 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Thermococcus celer
US-10-090-624-12
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288 ADIAYGA-----GRVNAYKAINYDNYAKLVFTGYVANKGSQTHQFVISGASFVTATLY 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 WDNAN-------GPLDLYLYDPNGNQ-VDYSYTAYY------GFEKVGYYNPTDG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 NLGYDGSGITIGIIDTGID-----ASHPDLQGKV-----IGWVDFVNGRSYPYDDHGHG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 HDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPK--PSLLKAALIAGA-----
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APPLICANT: TAKAKURA, Hikaru

APPLICANT: MORISHITA, Mio

APPLICANT: MORISHITA, Mio

APPLICANT: ASADA, Kayozo

APPLICANT: ASADA, Kayozo

APPLICANT: KATO, Ikunoshin

TILLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

FILE REFERENCE: TAKAURA=6

CURRENT APPLICATION NUMBER: US/10/090,624

CURRENT FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: 09/445,472

PRIOR APPLICATION NUMBER: 151969/1997

PRIOR APPLICATION NUMBER: 151969/1997

PRIOR FILING DATE: 1997-06-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin version 3.0

LENGTH: 522
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Publication No. US20020132335A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
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17.6%; Score 396; DB 13; Length 5.
Best Local Similarity 29.5%; Pred. No. 5.3e-26;
Matches 127; Conservative 56; Mismatches 163; Indels
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1 LOCATION: (428)...(428)

1 CHER INFORMATION: Xaa at position 428 is Gly or Val.

US-10-1090-624-4
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382 TWTIKVVSYS 391
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US-10-090-624-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 ADVGLGFPNGNQGWGRVTLDKSL---NVAFVNETSPLSTSQKATYSFTAQAGKPLKISLV 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 RIHTNSWGAPVNGAYTIDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAITVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 INDYYTAAPGTSMATPHVAGTAALLLQ-----AHPSWTPDKVKTALIETADIVKPDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 HDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGVTPK--PSLLKAALIAGA-----
                                                                                                                                                                                                                                                                                                                                                                                                          84; Gaps
                                                                                                                                                                                                                                                                                                                                                       Query Match 17.6%; Score 396; DB 13; Length 6
Best Local Similarity 29.5%; Pred. No. 7.3e-26;
Matches 127; Conservative 56; Mismatches 163; Indels
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Sequence 13251, Application US/10156761

Sequence 13251, Application US/10156761

SERERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIRAMA, UIN
APPLICANT: SHIRAM, HIROSHI
APPLICANT: SAKRI, YOSHITUKI
APPLICANT: SAKRI, YOSHITUKI
APPLICANT: APATORI MASHIRA
IITLE OF INVONTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PEPLICATION NUMBER: UF 2001-204089
PRIOR PELING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UF 2001-272697
PRIOR PLING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109
CURRENT APPLICATION NUMBER: US/10/090,62
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/445,472
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
US-10-090-624-16
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TWTIKVVSYS 523
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us-09-985-689a-7.rapb

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354 -SIGSPGAADSALTVGA------VDSSDRAAYFTSAGFRHGDNALKPDLAAPGVD 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 AA--LIAGAADVGLGFPNGNQGWG-RVTLDKSLNVAF-----VNETSPLSTSQKA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 DGEEVADRNGHGTHVTSTVGGSGAASDGTERGVAPGATLAVGKVLSDQGAG-----SESQ 294
                                                                                                                                                                                                                                                                                                                                                  112 TLFSQAYSA---CARIHTNSWGAPVNGAYTTD--SRNVDDYVRKNDMTILFAAGNEGPGS 166
                                                                                                                                                                                                                                                                                                                                                                             167 GTISAPGTAKNAITVGATENLRPSFGSYADNINHVAOFSSRGPTR-DGRIKPDVMAPGTY 225
                                                                                                                                                                                                                                                                     58 RINNANDPNGHGTHVAGSVLG-----NATNKGMAPQANLVFQSIM-DSGGGLGGLPANLQ 111
                                                                                                                                                                                          8 VKADVAQNN------FGLYGQGOIVAVADTGLDTGRNDSSMHEAFRGKITALYALG 57
                                                                                                             Query Match
15.8%; Score 355; DB 14; Length 1208;
Best Local Similarity 31.7%; Pred. No. 7.2e-22;
Matches 126; Conservative 51; Mismatches 151; Indels 70; Gaps
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; SEQ 1D NO 13251
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13251
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Search completed: March 31, 2004, 16:34:03 Job time : 34.1412 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 31, 2004, 15:58:38; Search time 11.3246 Seconds (without alignments) 3677.911 Million cell updates/sec

Title: Perfect score:

US-09-985-689A-7 2252 1 NDVARGIVKADVAQNNFGLY.......EVQAYNVFVSPQTFSLAIVH 433 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	multidrug resistan	818	rg Z	intracellular alka	microbial serine p	3.4	subtilisin-type pr	ne proteinas	yer-a	subtilisin (EC 3.4		alkaline serine pr	serine proteinase,	subtilisin-type pr	ğ	alkaline proteinas		ie proteina	high-alkaline seri	H	1-8	subtilisin (EC 3.4	n [import	ц	in send	pro	microbial serine p	ococcal C5a	microbial serine p
SUMMARIES		T18279	T18267	B83891	A69587	A41341	T28159	G83753	S11890	T29090	S23407	S25835	JC4908	D75393	C84120	A72647	3S0173	I39974	827501	A49778	A35742	F69730	I39780	G84406	871451	C69456	D86335	4133	3506	3986
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655 VDGYYPTGSIVESNKLQPTGSLLKALMINNAQLLNGTFQLITSSSITYPSNQVFENFAGA 714 304 --- QGWGRVTLDKSLNVAFVNETS------329

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JU0332 AI1930 T17093	A33973 SUBSCL A36734	T01351 D72593 A57690	139867 A42605 SUBSN JC4576	JC4802 S75976 JH0778
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## ALIGNMENTS

16;

Gaps

91;

Indels

Length 444;

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Clacesion: B83891

Strakam, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-4331, 200

A;Title: Camplete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A65650; MUD:20512582; PMID:11058132

A;Reference number: A83650; MUD:20512582; PMID:11058132

A;Reference number: DNA

A;References: DNA

A;Residues: 1-444 < CTO>

A;Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05649.1; GSPDB:GNO

A;Cross-references: strain C-125

G;Geneeics:
A;Genee: aprX
               infracellular alkaline serine proteinase aprX [imported] - Bacillus halodurans (strain C,Species: Bacillus halodurans C,Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVIRNGETLIGKDVTIAVIDIGI -----YPHEDLEGRIKAFVDFVNQREEPYDDNGHG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 DVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALY-ALGRINNANDPNGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
14.9%; Soore 334.5; DB 2;
Best Local Similarity 30.5%; Pred. No. 6e-15;
Matches 106; Conservative 50; Mismatches 100;
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T18267
multidrug resistance protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostellum discoideum
R;Shaulsky, G; Kuspa, A.; Loomis, W.F.
R;Shaulsky, G; Kuspa, A.; Loomis, W.F.
R;Shaulsky, G; Kuspa, Data Library, January 1995
A;Bescription: An MDR transporter/serine protease gene is required for prestalk speciality, A;Reterence number: Z18850
A;Accession: T1826
A;Accession: T1826
A;Accession: T1826
A;Accession: T1805
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                                 RDNGSTIFYSNQGGSSFLGLAPTQDTLNNVFGTVHNPTEPMTYRFMVAGTNVPMGPQNFS 889
                                                                                                             --- NWDGRNNVENVFINAPQSGTYTVEVQAYNVPVSPQTFS 428
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-----AQAGKPLK---ISLVWSDAPGSTTASLTLVNDLDLVITAPNGTKY
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llarity 28.1%; Pred. No. 8.8e-25;
Conservative 72; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAKNAITVGATENLRPSFGS-----YADNI-----
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                                                                                                             380 VGNDFTAPYDN-
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intracellular alkaline serine proteinase aprX - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Dibloc-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: A56587
C;Accession: A56587
C;Accession: A56587
C;Bron, S; Brouillet, S; Bruschi, C. V; Caldwell, B; Carter, N.M.; Ch
A; Ehrlich, S.D; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997 Fritz, C.; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Galle
A,Authors: Foulgar, D; Fritz, C.; Fujita, M; Fujita, X; Puma, S; Galizzi, A; Galle
A,Authors: Foulgar, D; Fritz, C.; Fujita, M; Kurita, K; Lapidus, A; Lardinois
A,Authors: Lauber, J; Lazarevic, S, Kumano, M; Kurita, K; Lapidus, A; Lardinois
A,Authors: Lauber, J; Lazarevic, V; Lee, S.M.; Levine, A; Liu, H; Masuda, S; Mause
Y, M; Ogawa, K,; Ogiwara, A; Oudega, B; Roche, B; Rose, M; Sadaie, Y; Sato, T; Scanlon
A,Authors: Schleich, S; Schroeter, R; Scoffone, F; Sekdyuchi, J; Sekowska, A; Scan
A,Authors: Schleich, A; Tanaka, T; Terpeira, F; Tosato, V; Tosato, V; Hohiyama
T; Winters, P; Wipat, A; Tanaka, T; Tryperstra, P; Tosato, M; Tosato, V; Hohiyama
T; Winters, P; Wipat, A; Tanaka, T; Tryperstra, P; Tosato, M; Y; Yoshida, A; Reference number: Aspance, C, the Gram-positive bacterium Bacillus subtilis.
A,Accession: A69580; MUID:98044033; PMID:9384377
A;Gcession: A69580;
A;Mclecule type: DNA
                                                                                   235
                                                                                                                                                                   161
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                                                                                                                                                                       --- DDYVR-----KNDMTILFAAGN
                                                         BGPGSGTISAPGTAKNAITVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 VTPKPSL----LKAALIAGA---AD-----VGLGF-----PNGNQ 304
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C.Species Bacillus subtilis
R.Slona, A: Ribo D. G.A. Therault, K.A.; Dwyer, M.; Wilson, S.W.; Pero, J.
J. Bacteriol. 173, 6889-6895, 1397
A. Filter Cloning and characterization of the gene for an additional extracellular serine
A. Reference number: A1341; MUDD:92041574; PMID:193892
A. Reference number: A1341; MUDD:92041574; PMID:1938892
A. Residues: 1-606 < SLO>
A. Residues: 1-61-195 < SLO>
A. Residues: 1
A;Residues: 1-442 <KUN>
A;Residues: 1-442 <KUN>
A;Cross-references: GB:Z99113; GB:AL009126; NID:g2634090; PIDN:CAB13610.1; PID:e1183385;
A;Cross-references: strain 168
C;Genetics:
C;Genetics: aprX
C;Superfamily: subtilisin homology
F;146-398/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 VAAGNSGPDSQTIASPGVSEKVITVGALDDNNTA----SSDDDTVASFSSRGPTVYGKEK 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 FAAGNEGPGSGTISAPGTAKNAITVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIK 216
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                                                                                                                                                                                                                                                                                                                                                             EVVRNGQTLTGKGVTVAVVDTGI-----YPHPDLEGRI----IĞPADMVNQKTEPYD 183
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30.9%; Pred. No. 9.5e-14;
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A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Winters, M.; Wibat, A.; Yamane, K.; Yasunoto, R.; Yoshida, A; Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.F.; Danchin, A. A; Reference number: A65980; MUID:98044033; PMID:9384377
A; Reference number: A65980; MUID:98044033; PMID:9384377
A; Rocession: D69730
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Rosidues: 1-806 «KUN»
A; Rosidues: 1-806 «KUN»
A; Rosidues: 1-806 «KUN»
A; Experimental source: strain 168
C; Comment: The amino terminal sequence of the mature protein and a molecular weight of C; Comment: The amino terminal sequence effect of the mature protein and a molecular weight of C; Superfamily: microbial serine proteinase vpr; subtilisin homology
C; Keywords: hydrolase; serine proteinase vpr; subtilisin homology
C; Keywords: hydrolase; serine proteinase predicted «Figo»
F; 128/Domain: signal sequence #status predicted «PRO»
F; 180-548/Domain: subtilisin homology #status atypical «SBT»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230
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SREAISVGATQLPLNEYAVTFGSYSSAKVMGYNKEDDVKALNNKEVELVEAGIGEAKDFE 396
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T28159
Pyrolysin (EC 3.4.-.-) - Pyrococcus furiosus
pyrolysin (EC 9.4.-.-) - Pyrococcus furiosus
C;Species: Pyrococcus furiosus
C;Species: Pyrococcus furiosus
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 24-Oct-2000
C;Accession: T28159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNNANDPNG----HGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---------NHVAQFSSRGPTRD-GRIKPDVMAPGTYILSAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 MUTAVILKDSDGEVYPHNAQGAG-----SARIMNAIKADSLVSPGSYSY----GTFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 DGEKLVSALKAGETKTTFKLTVSKALGEQVADFSSRGÞVMDTWMÍKÞÓISAÞGVNÍVSTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | ; | | | ; | | | : | | : DLGYTGKGYDFVDNDYDPKETPTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212;
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6.8e-13;
ches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 NFGLYGQGQIVAVADTGLDTGR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%; Score 309;
larity 23.2%; Pred. No. 6
Conservative 58; Mismatch
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nes 132, Conserv
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63

189;

799;

Length

228 512 288 561 343

--VAOFSSRGPT-RDGRIKPDVMAPGTYILS

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SVGAT----RLPYNKYKASVFTSDGIDYPSADIMGFPSDEELLELDGETYEYAFAGLGKPG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                              393 DFEGVDVEGKIALIVRGEIPFVEKAENAKAAGAVGAIIYNNVAGVQPTVPGLAIPTIMLS 452
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GYTGEGITVAILDTGVDYTHPD-----LVHARGDYKGWDFIDNNDDPQETPPG
                                                                                                                                                                                                                           453 NEDGLKMRNELENGQNTVTFSIEFDKLVGETVADFSSRGPVMHTWMIKPDVSAPGVAIVS
                                                                                                                                                                                                       DPNG----HGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS
                                                                                                                                                                                                                                                                                                                                        180 TVGATENLRPSFGSY-----ADNINH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 ARSSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIPTHQPDDPY-----GYGSRQGTSMASPHVAGAAALLLEAH-PNWGV----DHVKAAL
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                                                                                                                                    GLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGR-----TNN-----AN
                                                                                                                                                                                                                                                                                                         DGADIMNLSLGNTLNDPDFATSIAL-DWAMAEGVVAVTSNGNSGPNNWTVGSPGTSRDAI
C;Superfamily: microbial serine proteinase vpr; subtilisin
C;Reywords: hydrolase; serine proteinase
F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                   12.6%; Score 283.5; DB 2;
llarity 24.5%; Pred. No. 3.4e-11;
Conservative 48; Mismatches 127;
                                                                      Query Match
Best Local Similarity
Matches 118; Conserv
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       C.; Siezen, R.J.; Vos,
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                                                                                                                                                                                                                                                                                                                                                                                                                 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSAGARIHTNSWG--APVNGAYTTDSR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 FPNGNOGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTT 358
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                                                                                                                                                                                                                                                                                                                                                GNGYDIAYVOTDLDYDFTDEVPLGQYNVTYDVAVFSYYYGPLN--YVLAEI----DPNGE 354
                                                                                                                                                                                                                                                                                                                                                                                  84
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 R;Voorhorst, W.G.B.; Eggen, R.I.L.; Geerling, A.C.M.; Platteeuw, C.; Siezen, J. Babol. Chem. 271, 20426-20431, 1996
J. Biol. Cohem. 271, 20426-20431, 1996
A.Title: Isolation and characterization of the hyperthermostable serine prot A;Reference number: Z20481; MUD:96355370; PMID:8702780
A;Reference number: Z20481; MUD:96355370; PMID:8702780
A;Accession: T28159
A;Molecule type: DNA
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Acoss-references: EMBL:U55835; NID:g1556462; PID:g1556463; PIDN:AAB09761..]
A;Experimental source: DSM3538
C;Genetics:
A;Genetics:
A;Genetics:
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAA.----DVGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------NINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFWANHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     532 DYYGFYYFPAYTNV-RIAFFSSRGPRIDGEIKPNVVAPGYGIYSSLPMWIGGADF----
                                                                                                                                                                                                                                                                                                               ----SMHEAFRGKITALYALGRINNANDPN--
                                                                                                                                                                                                                                                                                                                                                                                  ------KG
                                                                                                                                                                                                                                                                                                                                                                                                               355 YAVFGWDGHGHGTHVAGTVAGYDSNNDAWDWLSMYSGEWEVFSRLYGWDYTNVTTDTVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVDDYVRKNDMT1LFAAGNEGPGSGT1SAPGTAKNA1TVGATENLRPSFGSYAD----
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                              Indels 160;
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                                                                                                                                                                                                                                             Length 1398;
                                                                                                                                                                                                                                                                                                                                                                                  -----GHGTHVAGSVLGNATN--------
                                                                                                                                                                                                                                            13.5%; Score 304; DB 2; Le 26.1%; Pred. No. 3.1e-12; ive 54; Mismatches 176;
                                                                                                                                                                                                                                                                                                                 GOGQIVAVADTGLDTGRNDS-----
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Les 138; Conservative
                                                                                                                                                                                                                                                                              Matches 138;
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Serine proteinase (EC 3.4.21.-) precursor, extracellular - Xanthomonas campestris. N.Alternate names: subtilisin-related proteinase (5.5pecies: Xanthomonas campestris pv. campestris (5.5pecies: Xanthomonas campestris pv. campestris (5.5pecies: Xanthomonas campestris pv. campestris (5.5pecies: Nov-1993 #sequence_revision 07-Feb-1997 #text_change 03-Dec-1999 R.Liu, Y.N.; Tang, J.L.; Clarke, B.R.; Dow, J.M.; Daniels, M.J. M.J. Genet. 220, 433-440, 1990 A.Title: A multipurpose broad host range cloning vector and its use to characteris A.Reference number: S11890; MuID:90251253; FMID:2187155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-580 < LiU>
A; Residues: 1-580 < LiU>
A; Residues: 1-580 < LiU>
A; Cross-references: EMBL: X51635; NID:948533; PIDN: CAA35962.1; PID:948534
A; Cross-references: Exanthomonas campestris pv. campestris
A; Note: the sequence from Fig. 4 is inconsistent with that from Fig. 3 in 1 C; Superfamily: subtlilisin; subtlilisin homology
C; Keywords: extracellular protein; hydrolase; serine proteinase
F; 1-32, Domain: signal sequence #status predicted <SIG>
F; 168-423/Domain: subtlilisin homology <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOGQIVAVADTGL----DTGRNDSSMHEAFRGKITALYALGRTNNAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.4%; Score 279.5; DB 2;
llarity 27.8%; Pred. No. 4.1e-11;
Conservative 49; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Db 664 TI-DGRGYGAQPDVFGGTSEATPYTSGTLALVFQAYKEVXNTTPDPVTAKIILKSS 718  Cy 292 AADVGLGFPNGNQWGRVTLDKSLNVAFVNETSPLSTSQXATYSFTAQAGKPL 344  T19 AKDIWYPAFSQGSGRVDALKAADTVFISEWLAVVSEGIQBAFLENYYTDFGPYTGYVL 776  Cy 345 KISLVWSDAPGST-TASLTLVNDLDLVITAPNGTKKVGNDFTAPYDNWDGRNNV 398  Db 777 PY-LADTDYYGVVKEGSSRNFTLNIVGNGAVSLSAWNTVLYKEYTV-YDGVYDYSG 830  Cy 399 ENVPINAPQSGTYTVEVQAYNVPVSPQTF 427  Db 831 -LLFLKVPKYAXSGADYVEVVVQLENMTYPPGVF 863	Accession: 523407  subtilisin (EC 3.4.21.62) 1 precursor - Bacillus sp. (strain TA39)  c.jspecides: Bacillus sp. c.jspecides: Bacillus sp. c.pate: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jun-1999 C;Accession: 523407 R;Narinx, E.; Pavail, 2.; Feller, G.; Gerday, C. Biochim. Biophys. Acta 1131, 111-113, 1992 A;Ritle: Nucleotide and derived amino acid sequence of the subtilisin from the a A;Reference number: \$23407; MUD:92256481; PMID:1581352 A;Accession: 523407 A;Molecule type: DNA A;Residues: 1-420 <nar> A;Residues: 1-420 <nar> A;Cross-references: EMBL:X62369; NID:940200; PIDN:CAA44227.1; PID:940201 C;Genetics:</nar></nar>	A;Gene: subl C;Guperfamily: subtilisin; subtilisin homology C;Guperfamily: subtilisin; subtilisin homology C;Guperfamily: subtilisin; subtilisin bydrolase; serine proteinase F;1-23/Domain: signal sequence #status predicted <sig>F;12-111/Domain: propebtide #status predicted <pro>F;12-420/Product: microbial serine proteinase #status predicted <mat>F;12-411/Domain: subtilisin homology <sbt>F;145,185,360/Active site: Asp, His, Score 266; DB 1; Length 420; F;145,185,360/Active site: Asp, His, Score 266; DB 1; Length 420; Best Local Similarity 31.4%; Pred. No. 2.1e-10; Best Local Similarity 31.4%; Pred. No. 2.1e-10; Matches 97; Conservative 40; Mismatches 114; Indels 58; Gaps 17; Cy 21 GGGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNGHGTHVAGS 75 Db 136 GGGINIAVLDTGVNINHPDLRNNVEQCKDFTVGTTYNNSCTDRQGHGTHVAGS 189 Cy 76 VLGNATNKGNAAPANIN-VFOSIMDSGCGLG-GLPANICTLFSGAYSACARIHTN- 127 Db 190 ALADGGTGNGY-YGVAPDADIMAXKVIGDDGSGYADDIAAARHAGDQATALNTKVVINM 248</sbt></mat></pro></sig>	OY 128 SWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGGGTISAPGTAKMAITVGATENL 187
65PNGHGTHSHADLNANILAGYDFISDATTARDGNGRDSNAADEGDWYAANECGA 227 65PNGHGTHVAGSVLGNATNKGMAPQANIV\	LD 312 LT 484 I- 371 VR 529 S 428 S 572	RESULT 9 T29090 Surface layer-associated STABLE proteinase - Staphylothermus marinus NiAlternate names: hyperthermostable proteinase C;Species: Staphylothermus marinus C;Sate: 02-Sep-2000 R;Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J. C;Accession: T20909 R;Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J. A;Title: A hyperthermostable protease of the subtilisin family bound to the surface laye A;Tatus: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: DNA A;Residues: 1-1145 cMAY> A;Coss-references: EMBL:U57968; NID:g1374755; PID:g1374756; PIDN:AAB02323.1 A;Experimental source: strain F1 C;Function: C;Function: A;Sperimental source and exodigestive function related to the organism's energy A;Note: stoichiometric S-laver component	Duery Match Best Local Similarity 27.3%; Score 277.5; DB 2; Length 1345; Best Local Similarity 27.3%; Pred. No. 1.7e-10; Matches 124; Conservative 66; Mismatches 157; Indels 107; Gaps 23;  46 FRGKITALYALGRINNANDPNGHCTHVAGSVLGNAINKGMAPQANLV 92  11

antarcti

predicted <CTP>

us-09-985-689a-7.rpr

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F;497-715/Domain: carboxyl-terminal propeptide #status predic
F;239-294,335-372,478-481/Disulfide bonds: #status predicted
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Matches 92; Conserv
                                                                                                     Query Match
Best Local Similarity
Matches 118; Conserv
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A,Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 GAGINIAVLDIGVNINHPDLSNNVEQCKD----FTVGTNFTDNSCTDRQGHGTHVAGSA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 LGNATN-----KGMAPQANL-VFQSIMDSGGGLG-GLPANLQTLFSQAYSAGARIHTN-SW 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAITVGATENLRP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 GSSGESSLIT---NAVDYAYDKGVLIIAAAGNSGPKPGSIGYPGALVNAVAALENTIQ 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
C;Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999 C;Accession: S25835
R;Davail, S.; Feller, G; Narinx, E.; Gerday, C.
Gene 119, 143-144, 1992
A;Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotr A;Accession: S25835
A;Accession: S25835
A;Molecule type: DNA
A;Accession: S25835, MUD:93012966; PMID:1398082
A;Molecule type: DNA
A;Cross-references: EMBL:X63533; NID:940198; PIDN:CAA45096.1; PID:940199
C;Superfamily: subtilisin; subtilisin homology
C;Superfamily: subtilisin; subtilisin predicted <8IG>F;1-23/Domain: signal sequence #status predicted <8IG>F;1-23/Domain: propeptide #status predicted <8IG>F;111-149/Product: microbial serine proteinase #status predicted <ART>F;135-373/Domain: subtilisin homology <BTP>F;144,184,359/Active site: Asp, His, Ser #status predicted
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Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999
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    Alteromonas

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.8%; Score 265; DB 1; Length 41 Best Local Similarity 30.9%; Pred. No. 2.4e-10; Matches 95; Conservative 39; Mismatches 119; Indels
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Gerine proteinase, subtilase family - Deinococcus radiodurans (strain R1)

(Species: Deinococcus radiodurans

(Species: Deinococcus radiodurans)

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A,Cross-references: GB.AE001990, GB.AE000513, NID:g6459214, PIDN:AAF11026.1, PID:g64592
A,Experimental source: strain R1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 VAAPG----GAQSFADDPEGILSTHNSGSGAPSNDSYHYSQGTSMAAPHVAGVAALIKQ- 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVKNRGVTPKPS-----LLK--AALIAGAADVGLGFPNGNQGWGRVTLDKSLNVAFV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497
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                                                                                                                                                                                                                                                                                                                                                                                                                      ANLQILFSQAYSAGARIHTNSWGAPV-----NGAYTTDSRNVDDYVRKNDMILFAAG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 NEGPGSGTISAPGTAKNAITVGAT--ENLRPSFGSYADNINHVAOFSSRGPTRDGRIKPD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 N-ETSPLSTSQKATYSFTAQAGKPLKISLVWSDAP-GSTTASLTL----VNDLDLVI---T 372
                                                                                                                                                                                      -NGHGTHVAGSVLGNATN----KGMAPQANLVFQSIMDSGGGLGGLP 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----SNCGTGVVDAAAAVNEALG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDIADGIIWASGGSDRVPANANPAVVINMSLGGGGACSATTONAINQARNNGTVIVIAAG
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                                                                          121;
                                                                                                                                         21 GQGQIVAVADTG----LDTGRNDSSMHEAFRGKITALYALGRTNNANDP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               558 OPTSSSY----DCRPYEG-----GNAEVCSFDAPQAGTYHVMINGY
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ilarity 28.0%; Pred. No. 7.3e-10;
Conservative 49; Mismatches 122;
11.7%; Score 262.5; DB 2; 25.3%; Pred. No. 7.4e-10; ive 51; Mismatches 176;
                                     ilarity 25.3%;
Conservative 5
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RKNDMTILFAAGNEGPGSG	Db 509 AKKLVDQEGVPHEIHEQGAGRIQVDKAVAATSLVYPGALSFGK 551
Db 273 SLGIPGTWINEFIVPVNIML-KAGVVPVFAIGNFGPAAGSTGSPGNLPQAIGVGA 325	CY 348 LVMSDAPGSTTASLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNW 392
QY 188 RPSFGSYADNINHVAQPSSRGPTR-DGRIKPDVMAPGTYILSARSSLAPDSSFWA 241	DD 552WAKDDLREKRPVTLTIENH-DTVKRTYHISPPFDVPDGVEW 591
242 NHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGL 297	RESULT 15 A72647 probable surface layer-associated STABLE proteinase APE0607 - Aeropyrum pernix (strain C;Species: Aeropyrum pernix
98 GFPNGNGGWGRVTLDKSLNVAFVNETSP 325 18KNNNVGFGGISIPGALGKLGVSTGTP 443	C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999 C;Accession: A72647 R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa, H.; Takamtya, M.; Masuda, S.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; awa, H.; Takamtya, M.; Masuda, S.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
-	DNA Res. 6, 83-101, 1999 A.Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A.Reference number: A72450; MUID:99310339; PMID:10382966 A.Accession: A72647
y] - Bacillus halodu nn-2001	A.Status: preliminary A.Molecule type: DNA A.Residues: 1.1331 AKAW> A.Residues: 1.1331 AKAW> A.Residues: 1.1331 AKAW>
1, N.; Fuji, F.; Hira	
A; Reference number: A83650; MUID:20512582; PMID:11058132 A; Accession: C84120 A; Status: preliminary A; Molecule type: DNA	Query Match Best Local Similarity 23.8%; Pred. No. 3.5e-09; Matches 107; Conservative 65; Mismatches 149; Indels 128; Gaps 19;
A;Residues: 1-757 <sto> A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07482.1; GSPDB:GN00 A;Experimental source: strain C-125 C;Genetics:</sto>	Qy 27 AVADTGLDTGRNDSSMHE-AFRGKITALYA
A;Gene: BH3763 C;Superfamily: microbial serine proteinase vpr; subtilisin homology C;Keywords: hydrolase; serine proteinase F;1-20/Domain: signal sequence #status predicted <sig></sig>	Oy 56LGRINMAN B2
Query Match 11.5%; Score 258; DB 2; Length 757; Best Local Similarity 22.6%; Pred. No. 1.6e-09; Matches 119; Conservative 56; Mismatches 156; Indels 196; Caps 20;	Qy 83 KGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSAG 121 
VKADVAQNNFGLYQGQIVAVADTGLDTGRNDSSMHBAFRGKITR 	Qy 122ARIHTNSWGAPVNGAYTTDSRNVDDY-VRKNDWTLLFAAGNEGFGSGTISAP 172 
OY 58 RTNNANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLÇTLFSQA 117  Db 177PPTLHGTHVSGIIAANGQVKGVAPEABIYAYRALGFGGQGTTEQVIAAIEKA 228	QY 173 GTAKNAITVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSAR 230
OY 118 YSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKN 177	Qy 231 SSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIA 290  Qy 231 SSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIA 290  Db 647VPVLTGLGNGSLAPDIFGGTSEATPMTSGSVALVISAYQQAFGAKPSPGLVKAILKS 703
Qy 178 AITVGAT	QY 291 GAADVGL-GFPNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQA 340  QY 104 PADPMGADEATYSFTAQA 340  OA 704 PADPMGADE
194	341 GKPLKISLYWSDAPGSTJASLILVNDL 367
Db 348 EGKVVLIKRGMVPFTEKVMHAVAAKARGVIIYNNTPGPFTGMIEGGVNIPVVSITREDGE 407	Db 760 PNPVEDTQIYPGVLKPGETAVETLVLKTL 788
QY 201	Search completed: March 31, 2004, 16:10:23 Job time : 12.3246 Becs.
QY 234 APDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAG 291	
OY 292 AADVGLGFPNGNQGWGRVTLDKSLNVAFVNETSPLSTSQXATYSFTAQAGKPLKIS 347	

pyrococcus bacillus su bacillus li bacillus pu thermoactin schizosacch

bacteroides caenorhabdi

trichoderma bacteroides

tritirachiu

P29142 P58502 P04189 P04189 P04081 P04081 P040903 P40903 P42780 P42780 P42780 P42780 P42779 P429779 P42779 P42779 P429779 P42979 P429

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R DictyBase; DB00001795; tagC.

R InterPro; IPR001393; AAA_ATPase.

R InterPro; IPR003493; AAA_ATPase.

R InterPro; IPR003493; ABC_transpt.

R InterPro; IPR00349; ABC_transporter.

R InterPro; IPR003409; Peptidase_S8.

R Pfam; PF000664; ABC_tran; 1.

R Pfam; PF00005; ABC_tran; 1.

R RPMNX; R00723; SUBTILIEN; 1.

R RPMNX; R00723; SUBTILIEN; 1.

R RPMOSITE; PS00011; ABC_TRANSPORTER 1; 1.

R RPGSITE; PS00131; ABC_TRANSPORTER 2; 1.

R PROSITE; PS00131; SUBTILASE_HIS; 1.

R PROSITE; PS00137; SUBTILASE_HIS; 1.

R PROSITE; PS00138; SUBTILASE_ESR; FALSE_NEG.

R PROSITE; PS00138; SUBTILASE_ESR; FALSE_NEG.

R PROSITE; PS00138; SUBTILASE_ESR; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SIMILARITY: In the N-terminal section; belongs to peptidase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).
-!- FUNCTION: Intercellular communication via tagC may mediate integration of cellular differentiation with morphogenesis (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1] — SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=AX4;
MEDLINE=97140317; PubMed=8986798;
Shaulsky G., Escalante R., Loomis W.F.;
"Developmental signal transduction pathways uncovered by genetic
                                                                                                                                                                                                                                                                                                                                                                                                                   01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Prestalk-specific protein tagC precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                     PRT; 1743 AA
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SUBIT BACST
TKGU PYRKO
SUBIT BACSU
SUBIT BACSU
SUBIT BACPU
THEAT THEVU
PRIT THEVI
BRX BACNO
SOGG CAREL
ALP
TATA
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TRIAL
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thermus cl
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bacillus su
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P54683 dictyosteli
P29141 bacillus su
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1 NDVARGIVKADVAQNNFGLY......EVQAYNVPVSPQTFSLAIVH
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                              141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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SUBA BICCI
PLES PYREU
EXPR XANCP
SUBT BACCSP
PROA VIBAL
THES BACCSP
BUSS BACLE
ISP BACCS
BLYA BACCS
ALIA BACCS
ALIA BACCS
ALIA BACCS
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RIVA BACCS
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WEA BACCS
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                     QKATYSFT-----AQAGKPLK---ISLVWSDAPGSTTASLTLVNDLDLVITAPNGTKY 379
655 VDGYYPTGSIVESNKLQPTGSLLKALMINNAQLLNGTFQLITSSSITYPSNQVFENFAGA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREMBI, T18267; T18267.

DR RENBI, T18267; T18267.

DR MEROPS, SOB.UPW; ---

DR MEROPS, SOB.UPW; ---

DR DictyBase; DDB001094; tedB.

DR InterPro; IPR001359; AAA_TPase.

DR InterPro; IPR001349; ABC_transporter.

DR InterPro; IPR000209; Peptidase_SB.

DR Pfam; PF000082; ABC_tran; 1.

DR Pfam; PF000082; ABC_tran; 1.

DR Prodom; DP000006; ABC_tran; 1.

DR Prodom; PP000006; ABC_transporter; 1.

DR Prodom; PP000006; ABC_transporter; 1.

DR PROSITE; PS0013; SUBTILISIN.

DR PROSITE; PS0013; SUBTILISIN 1.

PROSITE; PS00136; SUBTILASE_ASP; FALSE_NEG.

DR PROSITE; PS00136; SUBTILASE_ASP; FALSE_NEG.

PROSITE; PS00136; SUBTILASE_SER; 1.

RROSITE; PS00136; SUBTILASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: Intercellular communication via tagB may mediate integration of cellular differentiation with morphogenesis.
                                               715 SLVOGWGAIRMSNWLHVVNNNNSNNNNKTSDGITKFDGIGGLDLRLVKPNQWKEESLSTG
                                                                                                                                     S8.
--- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MDR SUBFAMILY.
--- SIMILARITY: STRONG, TO TAGC.
                                                                                             775 ONTSYCFTYKPSSSSSNSGNNIPRVVATLVWTDPPSYAGAKFNLVNNLDLIM-----IYY
                                                                                                                     380 VGNDFTAPYDN------NWDGRNNVENVFINAPQSGTYTVEVQAYNVPVSPQTFS
                                                                                                                                                                                                                                                                                                                                                      STRAIN=AX4;
MEDLINE=55262903; PubMed=7744252;
Shaulusky G., Kuspa A., Loomis W.F.;
"A multidrug resistance transporter/serine protease gene is required for prestalk specialization in Dictyostelium.";
Genes Dev. 9:1111-1122(1995).
                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-appecific protein tagB precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                ortyosteiium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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                         304 --- QGWGRVTLDKSLNVAFVNETS--
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27.0%; Pred. No. 9e-25;
ive 79; Mismatches 165; Indels 194; Gaps
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Db 787 VKSSNPTPPSRWIGIGGLGKNQKAT	Qy 344 -LKISLVWSDAFGSTTASLTLVNDL 	392	SULT 3	ACSU STANDAR		DE Minor extracellular protease vpr E GN VPR OR IPA-45R OR BSU38090.		RN 11) RP SEQUENCE FROM N.A., AND SEQUENCE C RX MEDLINE=92041574; Pubmed=1938892;	Sloma A., Kuro G.A. UI., Instruct Pero J., "Cloning and characterization of	RT extracellular serine protease of RRL J. Bacteriol. 173:6889-6895(1991).				RT "Bacillus subtilis genome project. RT kb region from 325 degrees to 333 RL Mol. Microbiol. 10:371-384(1993).		RA Aunst F., Ogasawara N., Moszer F., RA Azevedo V., Bertero M.G., Bessier RA Borriss R., Boursier L., Brans A. Pa Browiller S., Bruschi C.V., Caldw.	RA Choi S.K., Codani J.J., Connerton RA Denizot F., Devine K.M., Dusterho	RA Entian K.D., Errington J., Fabret RA Fritz C., Fujita M., Fujita Y., F RA Ghim S.Y., Glaser P., Goffeau A.,	RA Guiseppi G., Guy B.J., Haga K., H RA Hilbert H., Holsappel S., Hosono	RA Kobayashi Y., Koetter P., Konings RA Kurita K., Lapidus A., Lardinois	RA Lee S.M., Levine A., Liu H., Masu RA Medina N., Mellado R.P., Mizuno M RA Noone D., O'Reilly M., Oqawa K.,	RA Parro V., Pohl T.M., Portetelle D RA Presecan E., Pujic P., Purnelle B RA Rieger M., Rivolta C., Rocha E.,	RA Sato T., Scanlan E., Schleich S., RA Sekiguchi J., Sekowska A., Seror	RA Takeuchi M., Tamadkohi E., Tanaka T. Tanaka RA Takeuchi M., Tamadkoshi A., Tanaka RA Tosato V., Uchiyama S., Vandenbol	RA Viari A., Wambutt R., Wedler E.,
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Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REROPS; SOB.LFA; ...
REROPS; SOB.LFA; ...
RESUBLILIST: B2105911 vpr.
RESUBLILIST: B2105911 vpr.
RESUBLITIST: B2105911 vpr.
REPROPOSITY: PROUGES; Peptidase SB.
DR. INCEPTO: IPROUGESC: PA; 1.
DR. PETAN: PF00722; FURTILIASE SB; 1.
DR. PROSITE; PS00137; SUBTILIASE ASP; 1.
DR. PROSITE; PS00137; SUBTILIASE ASP; 1.
DR. PROSITE; PS00137; SUBTILIASE HIS; 1.
DR. PROSITE; PS00138; SUBTILIASE ZBRS; 1.
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(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                     Nature 390:249-256(1997).
-!- FUNCTION: NOT REQUIRED FOR GROWTH OR SPORULATION.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PIM: PROBABLY UNDERGOES C-TERMINAL PROCESSING OR PROTEDLYSIS.
-!- SIMILARITY: Belongs to peptidase family S8.
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EMBL; X73124; CAA51601.1; -.
EMBL; Z99123; CAB15835.1; -.
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HSSP; P00782; 2SBT.
MEROPS; S08.UPA; -.
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THE CHARACTERIZATION, AND 3D-STRUCTURE MODELING.

THE COST W.M., VOORhorst W.G.B., Dijkgraaf M., Kluskens L.D.,

A. Van der Oost J., Siezen R.J.;

A. Van der Oost J., Siezen R.J.;

The control characterization, and molecular modeling of pyrolysin and other extracellular thermostable serine proteases from the properties of the control of the con
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STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
MEDLINE=9635370; PubMed=8702780;
Voorhorst W.G.B., Eggen R.I.L., Geerling A.C.M., Platteeuw C., Siezen R.J., de Vos W.M.;
"Isolation and characterization of the hyperthermostable serine protease, pyrolysin, and its gene from the hyperthermophilic archaeon Pyrococcus furiosus.",
J. Blol. Chem. 271:20426-20431(1996).
                                                                                                                                                                                                564 MNTAVTLKDSDGEVYPHNAQGAG-----SARIMNAIKADSLVSPGSYSY----GTFL
517 PTHDPD------AKPKWSVEQISMASPHIAGAVAVIKQ------AKPKWSVEQIKAAI
                                                                                                         289 IAGAADV----GLGFPNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPL
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Pyrococcus.
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STRAIN=VOI / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss N.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus submitted (FEB-2002) to the EMBL/GenBank/DDbJ data
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28-FEB-2003 (Rel. 41, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Pyrolysin precursor (EC 3.4.21.-).
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EMBL, AE010153, AAL80411.1, -
PIR, T28159, T28159.
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Mol. Gen. Genet. 220:433-440(1990)
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                                                                                     PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Complete proteome.
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REDINE=2022145; PubMed=12024217;

REDINE=2022145; PubMed=12024217;

RA GINAR A.C.R., Ferro J.A., Reinach F.C., Camargo L.E.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Alves L.M.C., do Amaral A.J.S., Ferreira S.C., Camargo F., Ciapina L.P.,

RA Camarotte G., Cannavan R., Carreira R.C.C., Gruber A.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

RA Estuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Tornighieri E.C., Machado M.J., Madeira A.M.B.N., Martinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira W.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souca R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixaira B.C., Tezza R.I.D.,

RY Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RY Schubal J.C., Kitajima J.P.; two Xanthomonas pathogens with differing

RT host specificities "."

Nature 4171459-463 (2002).

CC -- SINLLARRIY: Belongs to peptidase family S8.
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                                                       245 SKYAYMGGISMAIPIVAGNVAQLREHFVKNRGVIPKPSLLKAALIAGAA-----DVGLG 298
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MEDLINE-90251253; PubMed=2187155;
MILLU Y.-N., Tang J.-L., Clarke B.R., Dow J.M., Daniels M.J.;
"A multipurpose broad host range cloning vector and its use to characterise an extracellular protease gene of Xanthomonas campestris
                                                                                                                                                                      FPNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTT
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=340;
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01-NOV-1991 (Rel. 20, Last sequence update)
01-RBS-2003 (Rel. 41, Last annotation update)
Extracellular protease precursor (EC 3.4.21.-)
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NCBI_TaxID=29336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 GIPAASSSWHGTHVAGTVAAVTNNTTGVAGTAYGAKVVPVRVLGKCGGSLSDIADAIVWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 FAAGNEGPG-SGTISAPGTAKNAITVGATEN--LRPSFGSYADNINHVAQFSSRGPTRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAAGNDASNVSG--SLPANCANVIAVAATTSAGAKASYSNFGTGI-------
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                                                                                                                                                                                                    InterPro,

Ream; PRO0122; Pep. ...

Ream; PRO0123; SUBTILISIN.

REALIS; PRO0123; SUBTILISIN.

REALIS; PRO0123; SUBTILIASE ASP; 1.

REALIS; PRO0136; SUBTILIASE ELIS; 1.

REALIS; PRO0137; SUBTILIASE ELIS; 1.

REALIS; PROOFER 3 3 7136 POTENTIAL.

FT PROPER 3 7137 S80 POTENTIAL.

FT CHAIN 7137 S80 EXTRACELLULAY RACTEASE.

FT ACT SITE 237 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT ACT SITE 409 409 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT ACT SITE 273 BY SIMILARITY.

FT ACT SITE 375 S80 SPOTENTIAL.

FT ACT SITE 409 409 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT ACT SITE 409 409 CHARGE RELAY SYSTEM (BY SIMILARITY).

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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.4%; Score 279.5; DB 1; 27.8%; Pred. No. 4.6e-11; iive 49; Mismatches 152;
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01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Subtilisin precursor (EC 3.4.21.62).
                                                                                                                             InterPro; IPR000209; Peptidase_S8.
InterPro; IPR000209; PPC.
InterPro; IPR009020; Protease inhib.
Pfam; PF00082; Peptidase_S8; I.
Pfam; PF04151; PPC; 1.
EMBL; AE012184; AAM40166.1;
PIR; S11890; S11890.
HSSP; PO7782; ZSBT.
MEROPS; S08.UPA; -.
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Marinx B., Davail S., Feller G., Gerday C.;

Tuloleotide and derived amino acid sequence of the subtilisin from

The antearctic psychrotroph Bacillus TA39.";

Biochim. Biophys. Acta 1131:111-113(1992).

L. FUNCTION: Subtilisin is an extracellular and peptide amides.

L. CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity

C. CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity

C. CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity

C. CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity

C. CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity

C. CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity

C. CATALYTIC ACTIVITY: Hydrolysis of proteins with broad secificity

C. CATALYTIC ACTIVITY: Hydrolysis of proteins with one of degrees of the Subtilisin is associated with onset of sporulation. However, subtilisin

C. CATALYTIC ACTIVITY: Hydrolysis on levels of subtilisin. However, subtilisin

C. SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBTILISH.
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CALCIUM (POTENTIAL).
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Fram, PF00082, Peptidase S8, 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE ASP, 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE ER; 1.
Hydrolase; Sporulation; Serine protesse;
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HSSP; Q99405; IMPT.
MEROPS; S08.UPA; -.
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420 AA;
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Matches 97; Conserv
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       104 GGLPANLQTLFSQAYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVR---KNDMT1LFAAG 160
                                                                                                                                                                          340 VFAPGSQIKSA------W--YDGGYKTISGTSMATPHVAG-VAAL--YLQENSSVS 384
                                300 NSNADACNYS-PARVATGVTVGSTTSTDARSFSNWGSCV-----D
                                                                                                                                                                                                                                NEGPGSGTISAPGTAKNAITVGAT - - ENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPD
                                                                                                                                        219 WAPGTYILSARSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVT
                                                                                                                                                                                                        279 PKPSILKAALIAGAADVGLGFPNGNQGWGRVTLDK-SLNVAFVNETS------
                                                                                                                                                                                                                                                                            -----PL---STSQKATYSFTAQAGKPLKISLVWSDAPGSTTASLTLVNDLD
                                                                                                                                                                                                                                                                                                 MEDLINE=20057863; PubMed=10588904; Smith C.A., Toogood H.S., Baker H.M., Daniel R.M., Baker E.N.; Smith C.A., Toogood H.S., Baker H.M., Daniel R.M., Baker E.N.; "Calcium-mediated thermostability in the subtilisin superfamily: the crystal structure of Bacilus Ak.1 protease at 1.8-A resolution."; J. Mol. Biol. 294:1027-1040(1999).
-!- COPACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MISCELLANEOUS: Has a pH optimum of 8.5, a temperature optimum of 75 degrees Celsius.
-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                 LVITAPNGTKYVGNDFTAPYDNNWDGR-----NNVENVFINAPQSGTYTVEVQAYN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from a
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Thermophilic serine proteinase precursor (EC 3.4.21.-) (Ak.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus sp. (strain AKI).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=95085262; Pubmed=7993087;
Maciver B., McHale R.H., Saul D.J., Bergquist P.L.;
"Cloning and sequencing of a serine proteinase gene
thermophilic Bacillus species and its expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.80 ANGSTROMS) OF 122-401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appl. Environ. Microbiol. 60:3981-3988(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 AA.
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InterPro; IPR009020; Protease Inhib.
Pfam; PF00082; Peptidase_S8; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L29506; AAA63688.1; -.
PIR; I39974; I39974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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NCBI_TaxID=1409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protease).
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NHDSKYAYMGGISMAIPIVAGNVAQLREHFVKNRGVIPKPSL------LKAALIAGAA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - FDGGYATISGTSMASPHAAGLAAKIWAQYPSASNVDVRGELQYRAYENDILSGYYAGYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 IVKADVAÇINI--FGL------YGQGQIVAVADTGLDTGRNDSSMHEAF
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=89326126; PubMed=2546861;
Deane S.M., Robb F.T., Robb S.M., Woods D.R.;
"Nucleotide sequence of the Vibrio alginolyticus calcium-dependent, detergent-resistant alkaline serine exoprotease A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALKALINE SERINE EXOPROTEASE A.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
84E96D9C649D4226 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%; Score 254; DB 1; Length 534;
26.1%; Pred. No. 1.9e-09;
ive 63; Mismatches 138; Indels 150;
                                                                                                                                                                                                                                                                                                                   01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
8-FSB-2003 (Rel. 141, Last annotation update)
Alkaline serine exoprotease A precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 76:281-288(1989).
-!- SIMILARITY: Belongs to peptidase family S8.
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POTENTIAL.
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InterPro; IPR000209; Peptidase_S8.
InterPro; IPR000200; Protease inhib.
Pfam; PF004151; Peptidase_S8; I.
Pfam; PF004151; Peptidase_S8; I.
PR08ITE; PS00136; SUBTILASE_ASP; I.
PROSITE; PS00137; SUBTILASE_HIS; I.
PROSITE; PS00138; SUBTILASE_HIS; I.
PROSITE; PS00138; SUBTILASE_ER; I.
PROSITE; PS00138; SUBTILASE_ER; I.
PROSITE; PS00138; SUBTILASE_ER; I.
PROSITE; PS00138; SUBTILASE_ER; I.
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Best Local Similarity 26.1
Matches 124; Conservative
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MEROPS; S08.050; -.
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534 AA,
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MEDINE=9842603; PubMed=9753430;

MEDLINE=9842603; PubMed=9753430;

Kuhn P., Krapp M., Solis S.M., Ganshaw G., Thoene M., Bott R.;

Kuhn P., Krapp M., Solis S.M., Ganshaw G., Thoene M., Bott R.;

Kuhn P., Krapp M., Solis S.M., Ganshaw G., Thoene M., Bott R.;

Rubtilisin.";

Enchemistry 37:13446-13452(1998)

C. I FUNCTION: Subtilisin is an extracellular alkaline serine protease,

It catalyzes the hydrolysis of proteins and peptide amides.

C. I CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity

for peptide bonds, and a preference for a large uncharged residue

C. I COPACTOR: Binds 2 calcium ions per subunit.

C. I COPACTOR: Binds 2 calcium ions per subunit.

C. SUBCELLULAR LOCATION: Secreted.

C. BHOTECHNOLOGY: Used as a detergent protease. Sold under the name

SAVInase by Novozymes.

C. I SUBCELLANBOUS: Secretion of subtilisin is associated with onset of

SOLUTARION, and many mutations which block sporulation at early
                                                                                                                                                                                                     66 --NGHGTHVAG---SVLGNATN-KGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 119
                                                                                                                                                                                                                           180 TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                                                                              AVGA------VDQYDRLASFSNYGTW-----VDVVAPGVDIVSTITG-----
                                                                                                                                14 ONNFGLY-----GOGGIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRINNANDP-
                                                                                                                                                                   137 QNTYIDYAWDVIKGSSGQEIAVIDIGVD-----YTHPDLDGKVIKGYDF--VDNDYDPM
                                                                                                                                                                                                                                                                                                     247 SGAEVINLSLGC---DCHTTTLENAVNYAWNKGSVVVAAAGNN--GSSTTFEPASYENVI
                                                                                                                                                                                                                                                                       AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crystal Structure of the alkaline proteinase Savinase from Bacillus lentus at 1.4-A resolution."; Mol. Biol. 223:427-445(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR.

STRUCTURE BY NMR.

MEDIINE=66184541; PubMed=8654411;

Remerowski M.L., Pepermans H.A.M., Hilbers C.W., van de Ven F.J.M.;

Radchone dynamics of the 269-residue protease Savinase determined

from 15N.NMR relaxation measurements.";

from 15N.NMR relaxation measurements.";

Eur. J. Biochem. 235:629-640(1996).
                                                                                                 58;
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                                                               Length 401;
                                                                                                 Indels
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01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Subtilisin Savinase (EC 3.4.21.62) (Alkaline protease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus lentus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1467;
                                42835 MW; 1C736EF4A89F256F CRC64;
                                                                                                   96;
                                                               11.1%; Score 249; DB 1;
31.7%; Pred. No. 2.8e-09;
iive 29; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
MBDLINE=92148829; PubMed=1738156;
Belzel C., Klupsch S., Papendorf G., Hastrup
Wilson K.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą
                                                                                                                                                                                                                                                                                                                                                                                                           240 WANHDSKYAYMGGTSMATPIVAGNVAQL 267
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                                                                                                   Conservative
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401 AA;
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                                                                 Query Match
Best Local Simil
Matches 85; C
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                                  SEQUENCE
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PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
PROSITE; PS0138; SUBTILASE SER; 1.
SIGNAI; 3D-Structure.
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CALCIUM 3.
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CALCIUM 1.
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CHARGE RELAY SYSTEM.
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EMBL, 527501, 527501.

EMBRODS; 508.030, ...

EMBL, 527501, 527501.

EMBL, 527501.

EMBL, 527501.

EMBL, 527501.

EMBL, 527501.

EMBL, 527501.

EMBL, 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 VKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRINNANDPNG
                                                                                                                                                                                                                                                                                                                                               25 HINSWGAPVNGAYTIDSRNVDDYVRKNDMILLFAAGNEGPGSGIISAPGIAKNAITVGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 E--NLRPSFGSYADNINHVAOFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 HDSKYAYMGGISMAIPIVAGNVA------QLREHFVKN 274
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STRAIN=221 / ATCC 21522 / JCM 9139 / DSM 2512;
Kato C., Nakano Y., Yamamoto M., Horikoshi K.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC'1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
intracellular alkaline protease (EC 3.4.21.-).
Bacillus clausi.
Bacteria, Firmicutes, Bacillales; Bacillaceae, Bacillus.
         259
261
267
269
2698 MW; 4D89F8778999BF8D CRC64;
                                                                                                                                                                                        10.9%; Score 245.5; DB 1; 31.0%; Pred. No. 2.8e-09;
                                                                                                                                                                                                                                                    32; Mismatches
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les 88; Conservative
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269 AA;
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P29140;
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stages affect expression levels of subtilisin. However, subtilisin is not necessary for normal sporulation.

-!- SIMILARITY: Belongs to peptidase family S8.

PDB; 1C9d; 06-0CT-99.

PDB; 1C9M; 10-JAN-01.

PDB; 1C9N; 10-JAN-01.

PDB; 1C9N; 10-JAN-01.

PDB; 1C9N; 11-UUL-01.

PDB; 1JAN; 11-UUL-01.

PDB; 1JAN; 14-OCT-96.

MEROPS; 508.103; --
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHACUM 1.
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                                                                                                                                                                                                                                                                                                 Interpro; IPR000209; Peptidase S8.
Interpro; IPR000209; Protease Inhib.
Interpro; IPR009201; Protease Inhib.
Pfan; PF00082; Peptidase S8; I.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00134; SUBTILASE ASP; I.
PROSITE; PS00134; SUBTILASE ERF; I.
PROSITE; PS00134; SUBTILASE ERF; I.
Hydrolase; Serine protease; Zymogen; Metal-binding; Calcium-binding; Signal; 3D-structure.
SIGNAL 1 27
PROPEP 28 112
alcalophilus presents a rigid fold with a flexible substrate-binding
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RELAY SYSTEM.
RELAY SYSTEM.
RELAY SYSTEM.
                                       Structure 5:21-524(1997).
1- COFACTOR: Binds 2 calcium ions per subunit.
-- SUBCELLUIAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to peptidase family S8.
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                                Structure 5:521-532(1997)
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                                                                                                                                                                                                                                                                                                                           302
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                                                                                                                             TNK---GMAPQANLVFQSIM--DSGGGLGGLPANLQTLFSQAYSAG--ARIHTNSWGAPV 133
                                                                                                                                                              157
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                                                                                    40 GAGQIIGVIDTGCQVDHPDLAERIIGGVNLTTDYG-GVETNFSDNNGHGTHVAGTVAAAE 98
                                                                                                                                                158 ----TDSEELHDAVKYAVSNNVSVVCAAGNEGDGREDTNEFAYPAAYNEVIAVGAVDFD
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                                  Gaps
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MEDLINE=91282483; PubMed=2059048;
van der Laan J.C., Gerritse G., Mulleners L.J.M., van der Hoek R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, characterization, and multiple chromosomal integration of Bacillus alkaline protease gene."; Appl. Environ. Microbiol. 57:901-909(1991).
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                                61;
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Mariani M., Schipper D., Boelens R.;
"The solution structure of serine protease PB92 from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
MEDLINE=930798250; PubMed=1447775;
Sobek H., Hecht H.-J., Aehle W., Schomburg D.,
"X-ray structure determination and comparison of two crystal
a variant (RanliSArg) of the alkaline protease from Bacillus
alcalophilus refined at 1.85-A resolution.";
J. Mol. Blol. 228:108-117(1992).
   Length 321;
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alkaline protease precursor (EC 3.4.21.-).
Bacillus alcalophilus.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1445,
10.9%; Score 245.5; DB 1; 30.4%; Pred, No. 3.5e-09; ive 40; Mismatches 114;
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(Rel. 23, Last sequence update)
(Rel. 42, Last annotation update)
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                              94; Conservative
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                 Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                           HGTHVAGSV--LGNATN-KGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSAGARI 124
                                                                                                                                                                                                                                                                        185 E--NLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFWAN 242
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                                                                                                                                                                                          122 VQAPAAHNR-GLIGSGVKVAVLDIGIST-----HPDLNIRGGASFVPGEP-STQDGNG
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STRAIN=221 / ATCC 21522 / JCM 9139 / DSM 2512;
MEDLINE=93043753; PubMed=1368952;
Takami H., Kobayashi T., Kobayashi M., Yamamoto M., Nakamura S. Aono R., Horikoshi K.;
"Molecular cloning, nucleotide sequence, and expression of the structural gene for alkaline serine protease from alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weinheim (1991).
-!- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                              65;
                                                             10.9%; Score 245.5; DB 1; Length 380;
.larity 31.0%; Pred. No. 4.4e-09;
Conservative 32; Mismatches 99; Indels 65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 HDSKYAYMGGTSMATPIVAGNVA------QLREHFVKN 274
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Microorganisms in alkaline evironments, pp.187-194, VCH,
Weinheim (1991).
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NCBI_TaxID=79880;
380
38853 MW; 539EA72771B6682C CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update
Alkaline protease precursor (EC 3.4.21.-).
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375 3
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                                                                                    Local Similarity
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DR InterPro; IPR0000209; Peptidase S8.

InterPro; IPR0000209; Procease Inhib.

BR InterPro; IPR0000209; Procease Inhib.

BR InterPro; IPR0000209; Procease Inhib.

BR FINITS; PR00135; SUBTILASE ASP; 1.

BROSITE; PS00136; SUBTILASE ASP; 1.

RESSITE; PS00136; SUBTILASE SER; 1.

WHYDROJES; Serine procease; Zymogen; Metal-binding; Calcium-binding;

W Hydrolase; Serine procease; Zymogen; Metal-binding; Calcium-binding;

T SIGNAL 1 27 POTENTIAL.

T PROPEP 28 111 ALXALINE PROTEASE.

T ACT SITE 143 143 CHARGE RELAY SYSTEM (BY SIMILARITY).

T ACT SITE 173 173 CHARGE RELAY SYSTEM (BY SIMILARITY).

T ACT SITE 1326 CHARGE RELAY SYSTEM (BY SIMILARITY).

T METAL 113 113 CALCIUM 1 (BY SIMILARITY).
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CALCIUM 2 (VIA CARBONYL OXYGEN)
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CALCIUM 2 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
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CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN)
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CALCIUM 1 (VIA CARBONYL
(BY SIMILARITY).
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31.0%; Pred. No. 4.4e-09;
iive 32; Mismatches 99;
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01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Aqualysin I precursor (EC 3.4.21..).
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SEQUENCE FROM N.A., AND SEQUENCE OF 15-23
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Best Local Similarity 31.0%;
Matches 88; Conservative 3
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P08594;
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243 -TRNHRRPAVANMSLGGGVSTA-----LDNAVKNSIAAGVVYAVAAGNDNANACNYS- 293
                                                                                                                                                                                                                                 230 RSSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTP---KPSLLKA 286
                                                                                                                                                                                                                                                      402 --LLSSGSGSTAPCTSCSYYTGSLSGPGDYNF---OPNGTYYYSPAGTHRAWLRGPAGTD 456
                                NDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMD--SGGGLGGLPANLQTLFSQAYSA 120
140 IDQRDLPLSNSYTYTATGRGVNVYVIDTGIRT-----THREFGGRARVGYDALG--GNG
                                                  121 GARIHTN-----SWGAPVNGAYTTDSRNVDDYVRKN----DMTILFAAGNEGPGSGTISA
                                                                                                                                                                 PGTAKNAITVGAT--ENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSA
                                                                                                                                                                                               294 PARVAEALTVGATTSSDARASFSNYGSCV-------DLFAPGASIPSA
                                                                                                                                                                                                                                                                                                 287 ALIAGAADVGLGFPNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKI
                                                                                                                                                                                                                                                                                                                                                                  SLVWSDAPGST-----TASLTLVNDLDLVITAPNGTKY-------VGND
                                                                                                                                                                                                                                                                                                                                                                                                                                      384 FTAPYDNNWDGRN------NVENVFINAPOSGTYTVEVQAYN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457 PDL-YLWRWDGSRWLTVGSSTGPTSEESLSYSGTAGYYLWRIYAYS 501
                                                                                                                                                                                                                                                                                                                                       382 ATTGRLSGIGSGSPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Q99405;
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PRIM BACSP
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                                                                                                                                                                                                                                                                                                                                                                                                    The optimal temperature for its caseinolytic activity is 80 degrees Celsius.

The optimal temperature for its caseinolytic activity is 80 degrees Celsius.

-!- SUBCELULAR LOCATION: Secreted.
-!- DEVELOPMENTAL STAGE: Secreted from the early stationary phase until the time the cells case to grow.
-!- PTM: THE N- AND C-TERMINAL PRO-SEQUENCES ARE REMOVED THROUGH THE PROTEOLYTIC ACTIVITY OF AQUALYSIN I ITSELF, IN THAT ORDER. THE C-TERMINAL PRO-SEQUENCES ARE REMOVED THROUGH THE PROTEOLYTIC ACTIVITY OF AQUALYSIN I ITSELF, IN THAT ORDER. THE PROTEASES ACROSS THE ORDER MEMBRANE.
-!- PTM: Two dismitide bonds are present.
-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.9%; Score 245.5; DB 1; Length 513; 26.0%; Pred. No. 6.5e-09; ive 43; Mismatches 145; Indels 157; Gaps
                   MEDLINE=90216674; PubMed=2182621; Terada I., Ohta T.; Terada I., Kwon S.-T., Miyata Y., Matsuzawa H., Ohta T.; Un'ique precursor structure of an extracellular protease, aqualysin I, with NH2- and COOH-terminal pro-sequences and its processing in Escherichia coli.";
                                                                                                                                                                                                                                                                                                   MEDLINE-88151937; PubMed=3162211;
Matsuzawa H., Tokugawa K., Hamaoki M., Mizoguchi M., Taguchi H.,
Terada I., Kwon S.-T., Ohta T.;
"Purification and characterization of aqualysin I (a thermophilic alkaline serine protease) produced by Thermus aquaticus XT-1.";
Bur. J. Biochem. 171:441-447(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                  STRAIN=TI;

MEDLINE=88225062; PubMed=3286255;

Kwon S.-T. Terada I., Matsuzawa H., Ohta T.;

Kwon S.-T. Terada I. Matsuzawa H., Ohta T.;

"Nucleotide sequence of the gene for aqualysin I (a thermophilic
alkaline serine protease) of Thermus aquaticus YT-1 and
characteristics of the deduced primary structure of the enzyme.";

Bur. J. Blochem. 173:491-497(1988).
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                                                                                                                                    SEQUENCE OF 75-442 FROM N.A., AND PARTIAL SEQUENCE.
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InterPro IPR009209, Protease Inhib.
Promo Procost Peptidase_88, 1.
PRNNTS, PR00723, SUBTILISIN.
PROSITE, PS00136; SUBTILIASE_ASP; 1.
PROSITE, PS00137; SUBTILIASE_HIS; 1.
PROSITE, PS00138; SUBTILIASE_HIS; 1.
PROSITE; PS00138; SUBTILIASE_RIS; 1.
Hyddrolase; Serine protease; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQUALYSIN I.
                                                                                                     J. Biol. Chem. 265:6576-6581(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53913 MW;
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HSSP; P06873; 2PRK.
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513 AA;
                                                                                                                                                                                                                                                                                       SEQUENCE OF 128-170
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                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).

Yamane T., Kani T., Hatanaka T., Suzuki A., Ashida T.,

Kobayashi T., Ito S., Yamashita O.;

"Structure of a new alkaline serine protease (M-protease)

Bacillus sp. KSM-K16.";

Acta Crystallogr. D 51:199-206(1995).
                                           01-FEB-1995 (Rel. 31, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
M-protease (EC 3.4.21.-).
Bacillus sp. (strain KSM-K.6).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
MCBI_TaxID=1409;
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269
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Pfam, PF00082; Peptidase_S8, 1.
PRINTS; PR00723; SUBTILASE_ASP; 1.
PROSITE; PS00136; SUBTILASE_HIS; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PRT;
                               01-FEB-1995 (Rel. 31, Created)
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62
215
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Best Local Similarity 26.0% Matches 121; Conservative

7 IVKADVAQNNFGLY---GQGQIVAVADTGLDTGRNDSSMHEAFRGKITALY-ALGRTNNA

24; 62

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RA Kunst F., Oggsawara N., Mosser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Broilet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Deviner K.M., Dusterhoft A., Erhilch S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Febret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kodayashi Y., Koetter P., Koningstein G., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Kumano M.,
RA Medina M., Liu H., Masuda S., Maule C., Medique C.,
RA Medina M., Mallado R.P., Mizuon M., Mosetl D., Nakai S., Noback M.,
RA Presecan E., Pujic P., Mizuo M., Mosetl D., Nakai S., Noback M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
R. Satto T., Scanlan E., Schleelle B., Rapoport G., Rey M., Takemaru K.,
RA Setiguchi J., Sekowska A., Satro E., Sin B.S., Schroeter R., Scotfone F.,
RA Takeuchi M., Tanaka H., Tanaka T., Taremaru K.,
RA Takeuchi M., Tanaka H., Tanaka T., Varsenoeger T.,
RA Takeuchi M., Tanaka H., Yamamoto M., Wannier F., Vassarotti A.,
RA Tosato V., Uchiyama S., Vandelder E., Wedler H., Wanner E.,
RA Yoshida K., Yoshikawa H.F., Zumacooi Et He Gram-positive bacterium Bacillus
R. The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                        WPRA_BACSU STANDARD; PRT; 894 AA.
P54433; 006726;
01-0071-996 (Rel. 34, Created)
115-DEC-1998 (Rel. 37, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Cell wall-associated procease precursor (BC 3.4.21.-) [Contains: Cell wall-associated polypeptides CWBP23 and CWBP52].
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Margot P., Karamata D.;
"The wprA gene of Bacillus subtilis 168, expressed during exponential
"The encodes a cell-wall-associated protease.";
Microbiology 142:3437-3444(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=168;
MEDLINE=98015415; PubMed=9353931;
Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.;
Medina N., Vannier F. Roche B., Autret S., Levine A., Seror S.J.;
Megenecing of regions downstream of adda (98 degrees) and citG (289
degrees) in Bacillus subtilis.';
Microbiology 143:3305-3308(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: NOT YET KNOWN; COULD BE INVOLVED IN PROTEOGLYCAN DEGRADATION, BY CLEAVAGE OF ITS PEPTIDE BRIDGES.
SUBCELLULAR LOCATION: Cell-wall bound.
PIM: PROCESSED INFO CWBP23 AND CWBP52.
                           206 --STYASLNGTSMATPHVAGVAALVKQKNPSWSNVQIRNH-LKN 246
                                                                                                                                                                                                                                                                                                                                                           Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                         [1] SEQUENCE FROM N.A., AND SEQUENCE OF 32-54 AND 414-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97158234; PubMed=9004506;
243 HDSKYAYMGGISMAIPIVAGNVA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=168;
                                                                                                                                                                  HGTHVAGSV--LGNATN-KGMAPQANLVFQSIMDSGGGLGGLFANLQTLFSQAYSAGARI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 HTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAITVGAT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E--NLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFWAN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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----DIVAPGVNVQSTYPG-----
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                                            (VIA CARBONYL OXYGEN)
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                                                                                       CARBONYL CAR
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264
268
269 AA;
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Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 565 S----RVLEFALKYAADKNVLIAAASGNDGENALSYPASSKYVMSVGAT------ 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 DNINHVAOFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFWANHDSKYAYMGGTSM 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610 NRMDMTÅDFSNYGKGL-----DISÅPGSDI----PSLVPNGN-----VTYMSGTSM 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    652 ATPYAAAAAGLL---FAQNPKLKRTEVEDMLKKT----ADDISFESVDGGEEELYDDYGD 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N----KGMAPQANLVPQSIMDSGGGLGGLPANLQTLFSQAYSAGARIHTNSWGAPVNGAY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 TTDSRNVDDYVRK--NDMTILFAAGNEGFGSGTISAPGTAKNAITVGATENLRPSFGSYA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 ATPIVAGNVAQLREHFVKNRGV--TPKPSLLKAALIAGAADVGLGFPNGNQ------ 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 IVAVADTGLDTGRNDSSMHEAFRGKITALYA---LGRTNNANDPNGHGTHVAGSVLGNAT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TAQAGK--PLKISLVWSDAPGSTTASLTLVNDLDLVITAPNGTKYVGNDFTAPYDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GWGRVTLDKSLNVAFVN-ETSPLSTSQKATYSF-------
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SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- DAKTSYKVVVVKGKPSGTPKVNAVKTKDTAVKGKANSKAMI 839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    765 KKLGSAKAGKDNAFKVNIA------TOKODOVLYLKATKG-
                                                                                                                                                                                                                                                 Subtlist; BGI1846; wprA.
InterPro; IPR000209; Peptidase_SB.
From Pr00082; Peptidase_SB. 1.
PRINTS; PR00723; SUBTLISSIN.
PROSITE; PS00136; SUBTLIASE_ASP; FALSE_NEG.
PROSITE; PS00137; SUBTLIASE_HIS; 1.
PROSITE; PS00138; SUBTLIASE_HIS; 1.
Hydrolase; Serine protease; Cell wall; Zymogen; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V -> A (IN REF. 1).
L -> I (IN REF. 1).
OF67C353E55F8DBC CRC64;
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(BY
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ilarity 23.8%; Pred. No. 1.8e-08;
Conservative 68; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARGE RELAY SYSTEM
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CHARGE RELAY SYSTEM
-!- SIMILARITY: Belongs to peptidase family S8.
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POTENTIAL.
CWBP52.
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96487 MW;
                                                                                                                                                        EMBL; US8981; AAC25926.1; -.
EMBL; Y09476; CAA70641.1; -.
EMBL; Z99109; CAB12917.1; -.
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894 AA;
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HSSP, Q45670, 1DBI.
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Matches 406; Conservative 19; Mismatches 8; Indels 1;
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Inch S., Saeki                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus sp. KSM-KP43.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=109322;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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X SEARIN-NVI;

X SEARINE-20568675; PubMed=11118284;

A SEARINE, Oxuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,

A HORIKOSHI K.;

"Novel oxidatively stable subtilisin-like serine proteases from
alkaliphilid Bacillus ssp.: enzymatic properties, sequences, and
arkaliphilid Bacillus ssp.: enzymatic properties, sequences, and
evolutionary relationships.";
Biochem. Biophys. Res. Commun. 279:313-319(2000).

-: SIMILANITY: BELDONGS TO PEPTIDASE FAMILY SB.

EMBL; ABO46406; BAB21269.1; -.

RESP; PO07082; 1SUP.

GO; GO:000823; F:spetidase activity; IEA.

GO; GO:000823; F:subtilase activity; IEA.

GO; GO:0008209; Peptidase SB.

InterPro; IPR00209; Peptidase SB.

InterPro; IPR007280; Peptidase SB.

Pfam; PF00082; Peptidase SB; 1.

Reference of the communication 
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=133781;
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01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
protease (Fragment).
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Matches 400; Conservative
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"Novel oxidatively stable subtilisin-like serine proceases from
"I "Novel oxidatively stable subtilisin-like serine processes from
"I alkaliphilic Bacillus sag.: enzymatic properties, sequences, and
evolutionary relationships.";

E shochem. Biophys. Res. Commun. 279:313-319(2000).

R RSP; PGOT62; 1SUP.
R GO; GO:0006289; Fsubtilase activity; IEA.
R GO; GO:0006289; Fsubtilase activity; IEA.
R GO; GO:0006209; Peptidase_S8.
InterPro; IPR007280; PPC.
R InterPro; IPR007280; PPC.
R Ffam; PF04151; PPC; 1.
R Pfam; PF04151; PPC; 1.
R PROSITE; PS00137; SUBTILASE_HIS; 1.
R PROSITE; PS00138; SUBTILASE_ERF; 1.
R SEQUENCE 639 AA; 68185 MM; 316AF6FFDBE4FF54 CRC64;
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Saeki K., Oktda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
Horikoshi K.;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=133778;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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421 VPQGPQAFSLAIVN 434
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Best Local Similarity 93.1%
Matches 404; Conservative
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Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami
Horikoshi K.;
   23; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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       386; Conservative
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NCBI_TaxID=127889;
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   NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 265
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MEDLINE=5D568(75; PubMed=11118284;
Sacki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
A HOTIKoshi K.;

"Novel oxidatively stable subtilisin-like serine proteases from
alkaliphilite Bacilius spp.: enzymatic properties, sequences, and
araliphilite Bacilius spp.: enzymatic properties, sequences, and
aroutionary relationships.";

Elochem. Biophys. Res. Commun. 279:313-319(2000).
-: SIMILANITY: BELDOMGS TO PEPPIDASE FAMILY SB.
EMBL; AB046405; BAB21268.1; -.
R HSSP; Q45670; IDBI.
GO: GO:0000823; F:peptidase activity; IEA.
GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
R GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
R INTE-PRO; IPR007296 Peptidase_SB.
R INTE-PRO; IPR007296 Peptidase_SB.
R FFEM: PF00082; Peptidase_SB: 1.
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Pred. No. 1.1e-111;
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=133780;
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PROSITE; PSO0137; SUBTILASE HIS; 1.
PROSITE; PSO0138; SUBTILASE_SER; 1.
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                      90.3%; Score 2033; DB 2; Length 433; 88.7%; Pred. No. 5e-111; ive 25; Mismatches 24; Indels
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Anjard C., Loomis W.F.;
Anjard C., Loomis W.F.;
Anjard C., Loomis W.F.;
Evolution of the ABC transporters of Dictyostelium.";
Submitted (AM-2002) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
R EMBL, AR465309; AAL74253.1;
--- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
R GO; GO:000524; F:ATP-binding; IEA.
R GO; GO:0000166; F:ATP-binding; IEA.
R GO; GO:0000166; F:MTP-binding cassette (ABC) transporter ac GO; GO:0000239; F:Profeeolysis and peptidolysis; IEA.
R GO; GO:0006508; P:Proceolysis and peptidolysis; IEA.
R GO; GO:0006508; P:Proceolysis and peptidolysis; IEA.
R InterPro; IPRO01140; ABC_IM_transpt.
                                                                                                         45587 MW; B81291A803C775AE CRC64;
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
serine procease/ABC transporter TagD.
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PROSITE, PS00138; SUBTILASE_SER; 1.
Hydrolase; Protease; Serine protease.
NON TER 1 1
NON TER 433 433
SEQÜENCE 433 AA; 45587 MW; B81291
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                                                                                                                                                         Query Match
Best Local Similarity 88.7%
Matches 384; Conservative
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                                                                                                                                                                                                 1 NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN 60
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Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
Horikoshi K.,
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                                                      Query Match
90.6%; Score 2040; DB 2; Length 433;
Best Local Similarity 88.9%; Pred. No. 2e-111;
Matches 385; Conservative 24; Mismatches 24; Indels
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Bacillus sp. Y.
Bacillus sp. Y.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NOBE_TaxID=133779;
     45636 MW; 52087E0A2516107F CRC64;
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
HSMEL, AB046404; BAB21267.1; --
HSSP; O45670; IDBI.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
INTERPRO; IPR007209; Peptidase_S8.
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Last annotation update)
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PROSITE; PS00137; SUBTILASE_HIS; 1.
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Pfam; PF04151; PPC; 1.
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01-UUN-2001 (TrEMBLrel. 17,
01-UUN-2001 (TrEMBLrel. 17,
01-UUN-2003 (TrEMBLrel. 24,
Protease (Fragment).
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           AA;
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        433
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        SEQUENCE
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Q9AQR2
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Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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Best Local Similarity
Matches 142; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 LREH-----FVKNRGVTPKPSLLKAALIAGAADVGLGFP------------------300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --PLSTSQ 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          725 ACANFVÓGWGSLRMSEWLYV----BSSGVKPKPSRWVGIGELGKDKKASNWKEYSLSTGQ 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----APNGTKYVGNDFTAPYDNNWDGRNNVENVF---INAPQSGTYTVEVQAYNVPVS 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DILVNNDRIDIPLRGKGQILSIADIGLDGSHCFFSDSNNPIPYNSVNLNHRKVVTYIGSL 374
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      InterPro; IPR003439; ABC transporter.
InterPro; IPR00209; Peptidase_S8.
Pfam; PF00064; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
Pfam; PF00082; Peptidase_S8; 1.
PRNMYS; PR00722; SUBTILIGIN.
PRODOM; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; I.
PROSITE; PS00211; ABC_TRANSPORTER_1; PROSITE; PS002137; SUBTILASE_HIS; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
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(TrEMBLrel. 16, I
(TrEMBLrel. 25, I
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                                                                                                                                                                                                                                                                                                                                               PROSITE; PS001
ATP-binding; SEQUENCE 182
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                                                                                                                                                    .; IEA
PSSIEKADPIINTGETNSYCFSLDSKADIDITLVWTDPAGSPLSTFTLVNNLDLALLAFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 GLYGOGOIVAVADIGLDIGR---NDSSMHEAFRGKITALYALGRINNANDPNGHGTHVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 GIKGDGEIVGCADTGIDINHCFFYDTNPIGSTHRKIIS-YSSGNGDQIDEIDGHGTHIVG
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123 RIHTINSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAITVG 182
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420 SWGPPSKNVDYGAGRLDGYEAIRVAGNFRGNNIDVPNHYYISGYLP-GSRYSDTWTFNAT 478
                                    339 QAGKPLKISLVWSDAPGSTTASLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 HDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPK--PSLLKAALIAGA-----
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                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422;

STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422;

Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

"The complete sequence of the Pyrococcus furiosus genome.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, ASO10255; AAL81794.1; - ...

GG; GG:0008233; F:peptidase activity; IEA.

GG; GG:0008233; F:peptidase activity; IEA.

GG; GG:000823; F:peptidase activity; IEA.

R GG; GO:000529; F:subtilase activity; IEA.

R GG; GO:000529; Peptidase S8; I.

R PROMOT2; PROMOT2; SUBTILISIN.

R PROSITE; PSO0136; SUBTILIASE ASP; I.

PROSITE; PSO0136; SUBTILIASE ASP; I.

PROSITE; PSO0137; SUBTILIASE ASP; I.

PROSITE; PSO0138; SUBTILIASE ESR; I.

PROCESSE (Complete protecome.

Protease; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 654;
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                                                              479 NTSYPIAITLIIPDWANYNP-----DFDIYLYDPSGTLIKSS---
                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.6%; Score 396; DB 17; 1
29.5%; Pred. No. 3.8e-15;
ive 56; Mismatches 163;
                                                                                                                                                                                                                                                 654 AA
                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                   522 ETITILPSQTGTYYVKVYSY 541
                                                                                                               399 ENVFINAPOSGTYTVEVQAY
                                                                                                                                                                                                                                                                                   (TrEMBLrel. 21, TrEMBLrel. 21, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.53
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                              Alkaline serine protease.
                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus furiosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                      01-JUN-2002 (
01-JUN-2002 (
01-JUN-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
                                                                                                                                                                                                            RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQNKDVYGIKVINLSLGTSTSSDGTDSTSLAVNRAVDSGIVVVVAAAGNSGPAKYTIGSPG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 TAKNALTVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APDSSFWANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVGLGFPNGNQGWGRVTLDKSLNVA------FVNETSPLSTSQKATYSFTA- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 TIPYDDNGHGTHVASIAAGTGAGNSFYKGVAPDALLVGIKVLDANGSGSMSTVTAGIDWA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 GIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNAN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----DPNGHGTHV----AGSVLGNATNKGMAPQANLVFQSIMDS--GGGLGGLPANLQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 FSQAYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPG
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=MB4 / JCM 11007;

MEDLINE=21992816; PubbMed=11997336;

A Chen Y., Xue Y., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

Bao Q., Tian Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

A Chen R., Wang J., Yu J., Yang H.;

A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002)

EMBL, AE011049; AAM24081.1; -

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0004289; F:subcilase activity; IEA.

GO; GO:0004289; F:hand.

R InterPro; IPR00209; Peptidase_S8.

InterPro; PR00920; Protease_inhib.

R Ffam; PF00161; PPC: Ill.

R Pfam; PF00161; PPC: Ill.

R Pfam; PF00161; PPC: Ill.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
17.9%; Score 404; DB 16; Length 561;
Best Local Similarity 30.2%; Pred. No. 1.1e-15;
Matches 133; Conservative 65; Mismatches 162; Indels 8
                                                                                                                                                                                                                                                                                 Thermoanserobacter tengcongensis,
Bacteria, Firmicutes, Clostridia, Thermoanserobacteriales,
Thermoanserobacteriacese, Thermoanserobacter,
NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease, Complete proteome.
SEQUENCE 561 AA; 59968 MW; BA9C5C52F7083A18 CRC64;
                                                                                                                                                                                    01-JUN-2002 (TrEWBLrel. 21, Created)
01-JUN-2002 (TrEWBLrel. 21, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
Subtilisin-like serine proteases.
                                                                                                                                                      561 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS, FROOTS, SUBTILLEIN.
PROSTIE, PSOCO18, EF HAND: 1.
PROSTIE, PSOCO18, SUBTILASE ASP; 1.
PROSTIE, PSOCO136; SUBTILASE HIS; 1.
PROSTIE; PSOCO138; SUBTILASE HIS; 1.
                                                                                                                                                      PRELIMINARY;
                                          : |
VVI 830
                                                                                                                                                                                                                                                                     APRE2 OR TTE0824.
                    LAI 431
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                    423
                                                                                                             RESULT
QBRBJ2
ID Q81
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Gaps

RESULT 11

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01-MAR-2001 (TIEMBLE). 16, Created)
01-MAR-2001 (TIEMBLE). 16, Last sequence update)
01-JUN-2003 (TIEMBLE). 24, Last annotation update)
Putative secreted peptidase.
SCOTISS OR SCSAII.16C.
                                                                                                                                                                                                                                       Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                          Streptomyces coelicolor
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es 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE 1239 AA
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                               STRAIN=A3(2);
Saunders D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3 (2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNSGPGDKTVGSPGISPKVITVGAADDNNTAERS----DDSVAEFSSRGPTIDGLTKPNL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 WCIQNQSKYNINIL---SLSLGSDATEPAEGDPVVNAVET------AWDNGMVVCVAA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 GNEGPGSGTISAPGTAKWALTVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 MAPGTYILSARS--SLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

WEDLINE=222076/7 PubMed=12235376;

WEDLINE=222076/7 PubMed=12235376;

A Takami H., Takaki Y., Uchiyama I.;

Takami H., Takaki Y., Uchiyama I.;

Takami H., Takami H., Uchiyama I.;

Tridge and its unexpected adaptive capabilities to extreme and its unexpected adaptive capabilities to extreme environments.";

Nucleic Acids Res. 30:3927-3935(2002).

UN Nucleic Acids Res. 30:3927-3935(2002).

UN Nucleic Acids Protocoly BACIANI.;

Nucleic Acids Protocoly Protocolysis and peptidolysis; IEA.

GO: GO:0006208; P:subtilase activity; IEA.

DR PROSITE; PRO00209; Peptidase S8.

DR PROSITE; PS00136; SUBTILASE ASP; 1.

DR PROSITE; PS00137; SUBTILASE ASP; 1.

DR PROSITE; PS00138; SUBTILASE ASP; 1.

R Complete protocome.

SQUENCE 430 AA; 45838 MW; 6D09A99BBCIE310F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                               ---GFEKVGYYNPTDG 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 DVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKIT -- ALYALGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 NNANDPNGHGTHVAGSVLGNAT----NKCMAPQANLVFQSIMDSGGGLGGLPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NLOTLFSQAYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes, Bacillales, Bacillaceae, Oceanobacillus.
NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.7%; Score 377; DB 16; Length 430; 34.7%; Pred. No. 2.8e-14; ive 44; Mismatches 122; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPKPSLLKAALIAGAADVGLGFPNGNQGWGRVTLDKSLNV 317
                                                                                                                                                                                                                                                                                                                         QBENVI;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Intracellular alkaline serine proteinase:
                            473 WDNAN-----SDLDLYLYDPNGNQ-VDYSYTAYY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T--PNQVKEKLMEACQDLGQS-PN-VQGAGYLNAANLINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
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Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oceanobacillus iheyensis
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                        410 TYTVEVQAYN 419
                                                                                                                           |:|::| :|:
514 TWTIXCVSYS 523
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Q9FBZ4;
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Q9FBZ4 ID Q9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 VKADVAQNNF-----GLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 VEADLADSTAQIGAPRAWAGGNIGQGVEVAVLDIGVDAG-----HPDLADRIAARQSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 RINNANDPNGHGTHVAGSVLGNAT----NKGMAPQANLVFQSIMDSGGGLGGLPANLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21996410; PubMed=12000953; MEDLINE=21996410; PubMed=12000953; MEDLINE=21996410; PubMed=12000953; Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Croin A., Farser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Olveil S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Hopwood D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:147(2002).
EMBL; A19391130; CACO1588.1; -...
HSSP; Q99405; 1MPT.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                             Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0004289; F: subtilase activity; IEA.
GO; GO:0006508; F: subtilase activity; IEA.
GO; GO:0006508; F: proteolysis and peptidolysis; IEA.
InterPro; IPR003137; PA.
InterPro; IPR00329; Peptidase_S8.
Ffam; PF00225; Pay 1.
Pfam; PF00225; Pay 1.
Pfam; PF0023; SUBTILISIN.
PROSITE; PS00134; SUBTILASE_HS; 1.
PROSITE; PS00134; SUBTILASE_HS; 1.
PROSITE; PS00138; SUBTILASE_HS; 1.
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Q82BI4;
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                                                         -----VDATDTLAPFSSQGPRVDGALKPEITAPGV 432
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332 MEWAAVERHAKIVNMSLGSGEQSDGSDPM-----SRAVDRLSAQTGALFVVAAGNGGE 384
                                                                                                                        433 GILAA-----NSSFAAGGNGAYOSLSGTSMATPHVAGAAALL-----AAARPDLS 477
                                                                                                                                                    285 KAAL---IAGAADVGLGFPNGNQGWGRVTLDKSLN-----VAFVNETSPLSTSQKATY 334
                                                                                                                                                                                                                                    538 INTIGAAVTLELSVAATHAPEGVFRLSASRVIVPAHGTÄDVTLIIDGS---GSAGGRAYS 594
                                         GSGTISAPGTAKNAITVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGT 224
                                                                                              225 YILSARSSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLL 284
                                                                                                                                                                               GSÁLKDVLÁSSSHRTPRYDAFQAGSGRVDVĎAAVRAGVYASATAYAPGSSPGPVRRLVTY
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BEDLINE-21996410, PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Cronin A., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Gobble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Stabbinowlisch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill JJ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Redenbach M., Kieser H.M., Denapaite D., Bichner A., Cullum J., Kinashi H., Hopwood D.A., Ast of ordered cognids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                  GNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNVPVSPQTFSL
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                  01-NAR-2001 (TrEMBLrel. 16, Created)
01-NAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Putative secreted peptidase.
SC07176 OR SC8A11.04C.
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MEDLINE=97000351; PubMed=8843436;
                                                           385 -AGSIGAPGVATSALTVGA-
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EMBL, AL939130; CAC01576.1;
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STRAIN=A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 MSLGDSPTDG---TDPLSEAVNWLSAETGALFVVAAGNSGPEAYTVGTPAAADAALTVGA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TENLRPSFGSYADNINHVAQFSSRGP-TRDGRIKPDVMAPGTYILSARSSLAPDSSFWAN 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387 PYDNNWDGRNNVENVFINA-----PQSGT------YTVEVQA-YNVPVSPQ 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LVITAPNGTKYVGNDFTA 386
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                 1253 AA; 130971 MW; AA69B417EFEEDB89 CRC64;
GO, GO.0008233; F.peptidase activity; IEA.
GO, GO.0006209; F.subtilase activity; IEA.
GO, GO.0006509; F.subtilase activity; IEA.
GO, GO.0006509; F.subtilase activity; IEA.
InterPro; IPR003137; PA.
InterPro; IPR003137; PA.
PERN; PP00225; PA; I.
PERN; PP00225; PA; I.
PERN; PP00325; PA; I.
PRNSITE; PS00134; SUBTILASE ASP; I.
PROSITE; PS00134; SUBTILASE ASP; I.
PROSITE; PS00135; SUBTILASE ASP; I.
PROSITE; PS00137; SUBTILASE EBR; I.
COMPLETE PS00137; MA; AA698417FFEEDBB9 CRC64
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SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  DB 16;
                                                                                                                                                                                                                                                                                                                                                             ; Score 367.5; DB 16;
; Pred. No. 4.1e-13;
60; Mismatches 171;
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NCBI_TaxID=33903;
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28.9%;
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25,
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Best Local Similarity 28.99
Matches 140; Conservative
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01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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MEDLINE=97144528; PubMed=8990295;
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                                                                                                      Streptomyces albogriseolus.
                                              FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 TLFSQAYSA---GARIHTNSWGAPVNGAYTTD--SRNVDDYVRKNDMTILFAAGNEGPGS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA--LIAGAADVGLGFPNGNQGWG-RVTLDKSLNVAF------VNETSPLSTSQKA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402 IRAARSOLAPGIGY-----YISMSGISMAIPHVAGVAALLAEQHPDWIGARLKDALMS 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455 TSEQLDASVYQLGAGRVSVPDAVGARVTATGSADLGFHRWPHDADRPVTKTVTYSNSSDT 514
                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                        58 RINNANDPNGHGTHVAGSVLG----NATNKGMAPQANLVFQSIM-DSGGGLGGLPANLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 VKADVAQNN------FGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALG
                                                                                     SEQUENCE FROM N.A.
STRAIN=RA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
MEDLINE=22608306; PubMed=12692562;
Sakaki Y., Ishikawa U., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilisi deducing the ability of producing secondary metabolitess.";
                                                                                                                                                                                                                                                                                                                                                  15.8%; Score 355; DB 16; Length 1208;
.larity 31.7%; Pred. No. 2.1e-12;
Conservative 51; Mismatches 151; Indels 70
                                                                                                                                                                                                                                                                                                                               1208 AA; 125548 MW; E650B5E3AEB5312B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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Best Local Similarity
Matches 126; Conserv
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SEQUENCE 1208 AA
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P95684;
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ID P9568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 TENLRPSFGSYADNINHVAQFSSRGP-TRDGRIKPDVMAPGTYILSARSSLAPDSSFWAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 ATGPKGKAAPAGFFTLGASTLTVPANGTASV--DVTADTRLGGAVDGTYSAYVVATGAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNGHGTHVAGSVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suzuki M., Taguchi S., Yamada S., Kojima S., Miura K., Momose "A novel member of the subtilisin-like protease family from
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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SEQUENCE 1102 AA; 114128 MW; F9E4AD2590FE559B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 179:430-438(1997).
-!- SIMILANTY: BELONGS TO PEPTIDASE FAMILY
EMBL; D98672; BAA12040.1; -.
HSSP; P00782; 2SBT.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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model	03 , Search time 47.1304 Seconds (without alignments) 2595.843 Million cell updates/sec
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ZSYS.843 MILLION CELL UDGGCE	US-09-985-689A-7 2253	1 NDVARGIVKADVAONNFGLYEVOAYNVPVSPOTFSLAIVH.43
	US-09-985-689	1 NDVARGIVKAD
	Title: US-0	Sequence:

33

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:*
geneseqp2001s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:* A_Geneseq_29Jan04:* 1: geneseqp1980s:* 2: geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Aaw89547 Bacillus Aaw89547 Bacillus Aay17090 Bacillus Aay17091 Bacillus Aay17091 Bacillus Aay17087 Bacillus Aay17087 Bacillus Aay17087 An alkali Aay17089 An alkali Aay17089 Bacillus Aaw50084 Bacillus Aaw50082 Bacillus Aaw50082 Bacillus Aaw5082 Bacillus Aaw89548 Bacillus Aaw56980 Bacillus Aaw61495 Modified Aaw95698 Bacillus Aaw46195 Modified Aaw95698 Bacillus Aaw46195 Modified Aaw46195 Modified Aaw46198 Bacillus An alkali An alkali Amino aci Description SUMMARIES AAW95698 AAY69207 AAY17089 AAW61495 AAR26274 AAY17091 Query Match Length DB 2252 212252 212252 212255 2112555 2111865 211665 206005 206005 1949.5 1649.4 1649.5 1649.5 432.5 396.3 2040 2038 Score Result No.

Aaw24122 Pyrococcu	Aaw94838 Hyperther	Aaw24129 Pyrococcu	Aaw94841 Hyperther	Aaw24123 Protease.	Abb09483 T. yonsei	Aab81180 Transglut		Aaw13666 Fragment	Aaw13667 Streptomy	Aaw13668 DhpA-mel	Abull343 Protein e	Aar27481 RP-III re	_	Aar87008 Protease.	Aaw24124 Pyrococcu	Aaw94839 WO9856926	Abp76735 Streptomy		Aay08471 F. balust
AAW24122	AAW94838	AAW24129	AAW94841	AAW24123	ABB09483	AAB81180	ABU07391	AAW13666	AAW13667	AAW13668	ABU11343	AAR27481	AAR87007	AAR87008	AAW24124	AAW94839	ABP76735	ABP76678	AAY08471
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17.6			17.6		16.4								13.6					19	
396	396	396	396	390	369.5	341.5	341.5	327.5	327.5	327.5	323	309	306	306	306	306	297	297	289
56	27	28	29	30	12.	35	33	34	35	36	37	38	ტ ტ	4	41	4	43	44	45

## ALIGNMENTS

RESULT 1

200	
T A G	AAANSUURK erandard, nrotein, 433 22
X	
AC	AAM50086;
×	
E À	12-AUG-2002 (first entry)
E H	Bacillus sp alkaline protease protein A-2 fragment.
X	4
Š	Alkaline protease; detergent; laundry; bleaching; dishwasher.
ğ	
SO	Bacillus sp.
ă	
NA ?	BP1209233-A2.
Ş	
Od:	29-MAY-2002.
ž	
7 5	ZZ-NCV-ZGOL; ZGOLEFF-UGLZ/8SI.
ž 8	22_MCVV_2000. 2000.TD_00255166
E C	
×	
PA	(KAOS ) KAO CORP.
X	
ΡĪ	
Ιď	Okuda M, Saeki K;
X	
DR	WPI; 2002-437518/47.
ž	
Ē	New modified alkaline proteases useful in detergent compositions.
X	
PS	Claim 5; Page 20-21; 25pp; English.
X	
ပ္ပ	This invention describes novel Bacillus sp. alkaline proteases useful in
ပ္ပ	
ပ္ပ	dete
ပ္ပ	to prior art alkaline proteases (31 and 23%).
ပ္ပ	sequence represents a fragment of the alkaline protease A-2 from Bacillus
បូ	sp NCIB12513 described in the method of the invention
>	

Sequence 433 AA; ΧS

Gaps 0 Query Match 100.0%; Score 2252; DB 5; Length 433; Best Local Similarity 100.0%; Pred. No. 1.2e-160; Matches 433; Conservative 0; Mismatches 0; Indels 0;

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WO9856926 Hyperther

Subtilase Subtilase

Aaw62230

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Novel protease from Bacillus subtilis LC20 - useful in laundry and dishwashing detergents and for leather processing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34. .208
/note= "prepro region"
209. .641
/note= "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US012005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-080908/07.
N-PSDB; AAV82382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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AMM99547
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This is the amino acid sequence of a novel protease of Bacillus sp. JP170 (NCIB 12513), as deduced from the nuclectide sequence of an isolated gene (see ANP62292). The entire protein, including the signal peptide and prepro region, has 77% identity to alkaline protease Y (see AAW89948) from Bacillus. The invention provides vectors, recombinant host cells and methods for the recombinant production of the protease. The protease is used in laundry and dishwashing detergents, for institutional and industrial cleaning, and for leather processing, as well as for choustrial cleaning, and for leather processing, as well as for hydrolysates, for flavour development through hydrolysis of proteins charactering and enhancing the degree of hydrolysis of proteins, degradation of undealied peptides and in enzymatic synthesis of peptides. It has enhanced stability towards oxidation under alkaline conditions, it is consistent conditions, provides mutant cells in which the protease activity is diminished. Such cells can be used for the production of heterologous recombinant proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAFGTAKNAIT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NANDENGHGTHAVAGSVLGNATNKGMAPQANTVPQSIMDSGGGLGGLPANLQTLFSQAYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVBVQAYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANHDSKYAYMJGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANHDSKYAYMGGISMATPIVAGNVAQIREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGNOGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alkaline protease; detergent; laundry; bleaching; dishwasher.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSM-KP43 alkaline protease protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 2252; DB 2; ilarity 100.0%; Pred. No. 2.1e-160; Conservative 0; Mismatches 0;
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  Page 53-54; 77pp; English
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Best Local Similarity
Matches 433; Conserv
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GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT
                                                                                                                                                                            GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGFGSGTISAFGTAKNAIT
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Kubota H,

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Saeki

Okuda M, Nomura M;

98WO-JP004528 97JP-00274570

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e protease, Bacillus, casein digestion, oleic acid, enzyme, composition, oxidising agent.
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N-PSDB; AAX37278.
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                                                                                             WO9918218-A1
                                                                                                                                            07-OCT-1998;
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                                                                                                                                                                                                                 Takaiwa M,
Shikata S,
                                  Alkaline
                                                                      Bacillus
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                                             washing
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                                                                                                                                                                                                            This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38$) compared to prior art alkaline proteases (31 and 22$). This sequence represents a fragment of the alkaline protease KP43 from Bacillus sp strain KSW-KP43 which is used to create the modified protease represented in AAMS/0902.
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94.4%; Score 2125.5; DB 5
Best Local Similarity 93.5%; Pred. No. 3.9e-151;
Matches 406; Conservative 19; Mismatches 8;
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                                                                                                          Sato
                                                                                                                                                                                         Claim 1; Page 10-11; 25pp; English
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                                                                                                          Kageyama
                      22-NOV-2001; 2001EP-00127851
                                             22-NOV-2000; 2000JP-00355166
12-APR-2001; 2001JP-00114048
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                                                                                                                                          WPI; 2002-437518/47
                                                                                                         Ogawa A,
Saeki K;
                                                                                 (KAOS ) KAO CORP.
                                                                                                                                                                                                                                                                                                             Sequence 434 AA;
29-MAY-2002
                                                                                                       Hatada Y,
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                                                                                                   The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by oleic acid and they have a high stability to oxidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range pH 6-12, (b) after 80% of of its optimum its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the bleaches. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.)
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protease from Bacillus used in washing powders.
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                                                         Disclosure, Page 58-63; 71pp; Japanese.
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(revised) (first entry)

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AGARIHTINSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGFGSGTISAPGTAKNAI
                                                                         387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVWAPGTFILSARSSLAPDSSF
                                                                                                             WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGF
                                                                                                                            300 PNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA
                                                                                                                                                                                   507 PNGNQGWGRVTLDXSLNVAYVNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA
                                                                                                                                                                                                                    360 SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                               AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI
                                                            TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alkaline protease; detergent; laundry; bleaching; dishwasher
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus sp KSM-KP9860 alkaline protease protein fragment.
                                                                                                                                                                                                                                                                                                                                                                   AAM50081 standard; protein; 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-2000; 2000JP-00355166.
12-APR-2001; 2001JP-00114048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-NOV-2001; 2001EP-00127851.
                                                                                                                                                                                                                                                                                                  627 VPVGPONFSLAIVN 640
                                                                                                                                                                                                                                                                       420 VPVSPQTFSLAIVH 433
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ogawa A,
Saeki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KAOS ) KAO CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus sp.
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Okuda M, S
                                                                                                                                                                                                                                                                                                                                                                                              AAM50081;
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           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by oles acidlus. The protease ability to digest casein is not inhibited by alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 6-11; (b) after 30 minutes at 40 dag. C it is stable over the pH range 6-11; (c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by 809-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the bleaches. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.)
              SVILVNDLDLVIIAPNGIQYVGNDFTSPYNDN#DGRNNVENVFINAPQSGTYTIEVQAYN 626
SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                                                                                                                                                                                                                                                                protease; Bacillus; casein digestion; oleic acid; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kageyama Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.2%; Score 2120.5; DB 2; Length 640; 93.3%; Pred. No. 1.6e-150; ive 19; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alkali protease from Bacillus used in washing powders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hitomi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kubota H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Japanese.
                                                                                                                                                                                                                                                                           washing composition; oxidising agent.
                                                                                                                                          AAY17091 standard, protein, 640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saeki K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 63-68; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                  98WO-JP004528
                                                                                                                                                                                                                                                                                                                                                                                                             97JP-00274570
                                                                            640
                                                  VPVSPQTFSLAIVH 433
                                                                                                                                                                                                                                     Bacillus alkaline protease
                                                                                                                                                                                              (revised)
(first entry)
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Matches 405, Conservative
                                                                  VPVGPQTFSLAIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okuda M,
Nomura M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-287736/27.
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                                                                                                                                                                                                                                                                                                                              WO9918218-A1
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21-JUL-1999
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                                                                                                                                                                    AAY17091;
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                       267
                                                 420
360
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                                                                                                                                                                             This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease KP9860 from Bacillus sp strain KSM-KP9860 described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                 New modified alkaline proteases useful in detergent compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.1%; Score 2118.5; DB 5; 93.3%; Pred. No. 1.3e-150; iive 18; Mismatches 10;
                                                                                                                               Page 12-13; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.3
Matches 405; Conservative
WPI; 2002-437518/47.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 434 AA;
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119 266

9

Gaps

1;

267 NANDINGHGIHVAGSVLGNGSINKGMAPQANLVPQSIMDSGGGLGGLPSNLQTLFSQAYS 326

NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN NANDPNGHGTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS

207 61

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1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN

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241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY 300
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                                                                                                                                                                                         61 NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLFSNVSTLFSQAYS 120
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                                                                                                                                                                                                                                                       121 AGARIHTUSWGAPVNGAYTTDSRNVDDYVRKNDMAVLPAAGNEGPNGGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                  TVGATENLR PSFGSYADNINHVAOFSSRGPTKDCRIKPDVMAPGTFILSARSSLAPDSSF
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                                                                                                           1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                            1 NDVARGIVKADVAQSSYGLYGGGQVVAVADTGLDTGRNDSSMHBAFRGKITAIYALGRTN
                                                                                                                                                                         NANDPNGHGTHVAGSVLGNAT - NKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS
                                                                                                                                                                                                                                    120 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                  TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                             Gaps
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Н
                                              Length 434;
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                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hitomi J,
                                                DB 5;
                                                                             12;
                                              Query Match
Best Local Similarity 92.2%; Pred. No. 1.9e-150;
Matches 400; Conservative 21; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kubota H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY17089 standard; protein; 639 AA.
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(first entry)
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Nomura M;
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N-PSDB; AAX37277.
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                  Sequence 434 AA;
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Shikata S,
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21-JUL-1999
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NDVARGIVKADVAQNNFGLYGQQQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                   NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                           NANDPNGHGTHVAGSVLGN-ATNKGMAPQANLVPQSIMDSGGGLGGLPANLQTLFSQAYS
                                                                                         NANDTNGHGTHVAGSVLGNGATNKGMAPQANLVFQSIMDSSGGLGGLPSNLQTLFSQAFS
                                                                                                                         AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI
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12-APR-2001; 2001JP-00114048.
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Saeki K,
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The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by oleic acid and they have a high stability to oxidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 9+6.12, (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-11, (c) its isoelectric point is 8.9-9.1, (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGS. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidiaing agents allows the bleaches. The present sequence represents an alkaline protease of the invention. (Updated on 20-MAR-2003 to correct DR field.)

    639
"note= "all residues indicated as Xaa are arbitrary amino
acids"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                          J, Кадеуата
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                             Alkali protease from Bacillus used in washing powders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                          Hitomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.5%; Score 2060.5; DB 2; 91.7%; Pred. No. 5.1e-146; iive 12; Mismatches 23;
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                                                                                                                                                                                                                                                                                            Kubota
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Location/Qualifiers
                                                                                                                                                                                                                                                                                            Saeki K,
                                                                                                                                                                           98WO-JP004528
                                                                                                                                                                                                                 97JP-00274570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 91.7
Matches 398; Conservative
                                                                                                                                                                                                                                                                                            Okuda M,
Nomura M;
                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-287736/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 639 AA;
                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX37277
    Key
Misc-difference
                                                                                                                                                                           07-OCT-1998;
                                                                                                                                                                                                                 07-OCT-1997;
                                                                                                WO9918218-A1
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                                                                                                                                                                                                                                                                                              Takaiwa
                                                                                                                                                                                                                                                                                                                 Shikata
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                                                                           Bacillus. The proceases ability to digest casein is not inhibited by oleic acid and they have a high stability to oxidising agents. The stability to oxidising agents. The is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 6-11; (b) after 30 minutes at 40 deg; (i is stable over the pH range 6-11; (c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proceases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the bleaches. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNGNOGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVILVNDLDLVITAPNGTRYVGNDFSAPFDNNWDGRNNVENVFINSPQSGTYTIEVQAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NANDPNGHGTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVYKNRGVTPKPSLLKAALIAGAADVGLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNERPNGGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alkaline protease; Bacillus; cassin digestion; oleic acid; enzyme; washing composition; oxidising agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An alkaline protease sequence from Bacillus species.
                                                                                                                                                                                                                                                                                                                                                                                              93.7%; Score 2110.5; DB 2; 93.1%; Pred. No. 9e-150; ive 18; Mismatches 11;
                         Disclosure; Page 53-58; 71pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPVSPQTFSLAIVH 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      404; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                           Sequence 639 AA;
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21-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY17087;
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This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease SD-521 from Bacillus sp strain SD-521 (FERM BP-11162) described in the method of the
                                                                                                                                                                                                                                                                                                                                    387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTXILSARSSLAPDSSF
                                                                                                                                                                                                                                                                      (FERM BP-11162) alkaline protease protein fragment.
                                                    AGARIHINSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI
                                                                             AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEXPNGGTISAPGTAKNAI
                                                                                                                                                                                  WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGF
                                                                                                                                                                                                                447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADXGLGY
                                                                                                                                                                                                                                                   PNGNOGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA
                                                                                                                                                                                                                                                                                                                  SLILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                                                                                                                    180 TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified alkaline proteases useful in detergent compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alkaline protease; detergent; laundry; bleaching; dishwasher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 16-18; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kageyama Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM50084 standard; protein; 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-NOV-2000; 2000JP-00355166.
12-APR-2001; 2001JP-00114048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-2001; 2001EP-00127851
                                                                                                                                                                                                                                                                                                                                                                                     VPVSPQTFSLAIVH 433
                                                                                                                                                                                                                                                                                                                                                                                                                     VPVGPOXFSLAIVN 640
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Saeki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-437518/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
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                        267
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                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 1. .640 /note= "all residues indicated as Xaa are arbitrary amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NANDPNGHGTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by oleic acid and they have a high stability to exidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 6-11; (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the bleaches. The present sequence represents an alkaline protease of the invention. (Updated on 20-MAR-2003 to correct DR field.)
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                                                                                                                                                                                                                                                                                    Alkaline protease, Bacillus, casein digestion, oleic acid, enzyme, washing composition, oxidising agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kageyama
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                                                                                                                                                                                                                                                      An alkaline protease sequence from Bacillus species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hitomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.5%; Score 2060.5; DB 2; 91.7%; Pred. No. 5.1e-146; ive 12; Mismatches 23;
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                                                                                                                                       AAY17088 standard; protein; 640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saeki K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-JP004528
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                          433
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(first entry)
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                                               VPVGPQXFSLAIVN
                          VPVSPQTFSLAIVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okuda M,
Nomura M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease from
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N-PSDB; AAX37278.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9918218-A1
                                                                                                                                                                                                                                                                                                                                      Bacillus sp
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                                                                                                                                                                                                       20-MAR-2003
21-JUL-1999
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                        420
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Shikata !
                                                      626
                                                                                                                                                                         AAY17088,
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361 YILVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYTIEVQAYNV 420
                                                                                                                                                                                                                                                                                                                  VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW 240
                                                                                                                                                                                                                                                                                                                                                                                                                              301 NGNQGWGRVTLDKSLNVAPVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTAS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease E-1 from Bacillus sp strain D6-(FPRM-P1592) described in the method of the invention
                                                                                                                                                                                                                        LTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNV 420
                                                                                                                                                                                                   NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 120
                                                                                                                                                                                                                                                                                                                                                                         ANHOSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
                                                                                                                                                                                                                                                                                                                                           VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
                                                                                                                                                                                                                                                                                                                                                                                        1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                  1 NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                                                                                            GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel protease from Bacillus subtilis LC20 - useful in laundry and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detergent; surfactant; leather processing;
                                                                                           Length 433;
                                                                                                                      Indels
                                                                                        90.6%; Score 2040; DB 5;
llarity 88.9%; Pred. No. 1e-144;
Conservative 24; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus sp. alkaline protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSGPORFSLAIVH 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Christianson L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alkaline protease Y;
debittering; flavour.
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                                                                                                    Local Similarity
es 385; Conserv
                                                                 Sequence 433 AA;
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                                                                                           Query Match
                                                                                                          Best Loc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $
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                                                                                                                                                                                                                  VGATENLRPSFGSYADNINHVAOFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW
                                                                                                                                                                                                                                      181 VGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
                                                                                                                                                                                                                                                                                            ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP
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                                                                                                                                                                                                                                                                                                                                  NGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTAS
                                                                                                                                                                                                                                                                                                                                                    LILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNV
                                                  1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                ANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
                                                                            NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                          NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA
                                                                                                                                                               GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGFGSGTISAFGTAKNATT
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                          Indels
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                          23;
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             5.2e-145;
           Pred. No. 5.26
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 13-15; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        >
standard; protein; 433
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12-APR-2001; 2001JP-00114048
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                       Conservative
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Saeki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-437518/47
        Best Local Similarity
Matches 386; Conserv
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                                                                                                                                                                                                                                                                                                                                                          Okuda M,
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                                                                                                           This is the amino acid sequence of a Bacillus sp. alkaline protease Y that is said to have good alkali and surfactant resistance and improved detergency. It shows 7% identity to a newly isolated protease (see AAW8547) of Bacillus sp. JP170 (NCIB 12513). The invention provides production of such proteases. The protease are used in laundry and isolahwashing detergents, for institutional and industrial cleaning, and for leather processing, as well as for debittering and enhancing the for leather processing, as well as for debittering and enhancing the chrough hydrolysis of protein hydrolysates, for flavour development through hydrolysis of proteins, degradation of undesired peptides and in enzymatic synthesis of proteins, e.g. towards bleaching agents of the protease activity is diminished. Such cells can be used for the protease activity is diminished. Such cells can be used for the production of heterologous recombinant proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636;
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for leather processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.5%; Score 2038; DB 2;
88.9%; Pred. No. 2.5e-144;
ive 25; Mismatches 23;
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                                                              Page 55-56; 77pp; English
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      detergents and
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hes 385; Conservative
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Best Local Simil
Matches 385; (
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dishwashing
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                                                           Claim 3;
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                                                                                                                                                                                                                                                                               New modified alkaline proteases useful in detergent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.3%; Score 2033; DB 5; Best Local Similarity 88.7%; Pred. No. 3.5e-144; Matches 384; Conservative 25; Mismatches 24;
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                                                                                                                                                                                Sato T,
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                                                                                                                                                                                                                                                                                                                        Claim 5; Page 15-16; 25pp; English
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2001JP-00114048
                                      22-NOV-2001; 2001EP-00127851
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Saeki K;
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                                                                                                                                     (KAOS ) KAO CORP
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29-MAY-2002
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Alkali-protease Ya enzyme

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                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of alkali-protease Ya enzyme which can be used in the recombinant production of Ya enzyme. Ya enzyme is excellent in alkali resistance and surface active agent resistance and improves detergency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 SGDGGWGRVILDKSLNVAYVNEATALAIGQKAIYSFQAQAGKPLKISLVWTDAPGSTIAS 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GARIHTNSWGAPVNGAYTANSRQVDETVRNNDMTVLFBAGGNEGPNSGTISAPGTAKNAIT 180
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                                          Alkali resistance, surface active agent resistance, detergency improver.
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                                                                                                                                                                                                                                                                                            DNA coding alkali-protease Ya enzyme - has good alkali and surfactant resistance and improves detergency.
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90.2%; Score 2032; DB 2; Length 4:
Best Local Similarity 88.7%; Pred. No. 4.1e-144;
Matches 384; Conservative 25; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 1; 17pp; Japanese.
                                                                                                                                                              90JP-00327110.
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                                                                                                                                                                                                                     (LIOY ) LION CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 433 AA;
                                                                      Bacillus sp. Y.
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Search completed: March 31, 2004, 16:04:34 Job time: 48.1304 secs

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Sequence 8, M Sequence 6, M Sequence 2, M Sequence 44, M Sequence 4, M Sequence 4, M Sequence 4, M Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 1

Sequence

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1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSWHEAFRGKITALYALGRIN
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Sequence 42, Application US/08873478

Sequence 42, Bapplication US/08873478

Patent No. 5893701

APPLICANT: Slowa, Alan
APPLICANT: Lynna, Christianson
TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Procease Activity
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58917010 No. 5891701disk of No. 5891701th A
STREET: 405 Lexington Avenue

CIIY: New York
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FILING DATE: 12-UN-1997
CLASSIFFCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 5251.000-US
TELEPHONE: 212-667-0123
TELEPHONE: 212-667-0123
                                                                        US-09-445-472-6
US-08-750-532-18
US-09-966-9212-18
US-08-873-479-44
US-08-254-021-4
US-08-258-798-4
US-08-585-798-4
US-09-585-798-4
US-09-585-798-4
US-09-585-798-4
US-09-585-798-4
US-08-566-369-11
US-09-70-70-70-11
US-07-76-691G-5
US-08-254-021-5
                                                 -08-894-818B-8
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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Best Local Similarity 100.
Matches 433; Conservative
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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OPERATING SYSTEM:
STRANDEDNESS:
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Sequence 6, Appli
                                                                                                                                                                             March 31, 2004, 15:59:39 ; Search time 13.9892 Seconds (without alignments) 1597.947 Million cell updates/sec
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1. /ogn2 6/ptodata/2/iaa/5A COMB.pep:*

2. /cgn2 6/ptodata/2/iaa/5B COMB.pep:*

3. /cgn2 6/ptodata/2/iaa/6A COMB.pep:*

1. /cgn2 6/ptodata/2/iaa/6B COMB.pep:*

2. /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*

3. /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*

3. /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-509-814A-4
US-09-509-814A-4
US-09-509-814A-1
US-09-509-814A-1
US-09-104-52A-4
US-09-104-52A-4
US-09-512-12A-10
US-09-512-25A-10
US-09-512-25A-10
US-09-512-25A-10
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US-09-445-472-12
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US-09-514-340-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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       327 AGARIHINSWGAAVNGAYTIDSRNVDDYVRKONDWTILFAAGNBGPNGGTISAPGTAKNAI 386
                                                                                                                                                              387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 446
                                                                                                                                                                                                                                                           240 WANHDSKYAYMGGTSMATFIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGF 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
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                                                                                                                    TVGATENLRPSFGSYADNINHVAOFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                      447 WANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY
                                                                                                                                                                                                                                                                                                                                                                                                   300 PNGNOGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KAGENAMA, YASUSHI
APPLICANT: KAGENAMA, YASUSHI
APPLICANT: KAGENAMA, SHITSUW
APPLICANT: NOWURA, MASAFUMI
I TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0337-032-09CT
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DFT/JP98/04528
PRIOR APPLICATION NUMBER: JP9-10-07
PRIOR APPLICATION NUMBER: JP9-274570
PRIOR FILING DATE: 1997-06-08
NUMBER: OF SEQ ID NOS: 24
SEQ ID NOS: 24
SEQ ID NOS: 24
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Patent No. 6376227
GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIKIO
APPLICANT: OKUDA, MITSUYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 VPVSPQTFSLAIVH 433
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APPLICANT: SABKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
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Best Local Similarity
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                                                                                                                                                                                                                                                                           329 GARIHTINSWGAPVNGAYTTDSRNYDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT 388
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209 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 268
                                                                             NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 120
                                                                                                                                               269 NANDPNGHGTHVAGSVLGNATNKGMAÞQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 328
                                                                                                                                                                                                                 GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT 180
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APPLICANT: CKUDA, MITSIYOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: SHIKATA, YSGUSHI
APPLICANT: SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA,
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Matches 406; Conservative
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US-09-509-814A-6
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360 SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 419
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APPLICANT: TAAANA, MIKIO
APPLICANT: GNUDA, MITSTYOSHI
APPLICANT: SARKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: KUBOTA, HIROMI
APPLICANT: KAGBYAM, YASUSHI
APPLICANT: HITOMI, JUN
APPLICANT: SIHKATA, SHIKUW
APPLICANT: SIKATA, SHIKUW
APPLICANT: SIKATA, SHIKUW
APPLICANT: SOMERA, MASARUMI
TITLE REFERENCE: 0327-0822-0PCT
CURRENT APPLICATION NUMBER: US/09/509, 614A
CURRENT ALING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VERSION 3.0
SECTION IN 18
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LOCATION: (23)—(23)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (29)—(29)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (32)—(32)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (42)—(44)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (47)—(46)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (47)—(47)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (47)—(47)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (47)—(43)
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NAME/KEY: misc feature
LOCATION: (105). (105)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (128).. (128)
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NAME/KEY: misc feature
LOCATION: (102)..(102)
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NAME/KEY: misc_feature
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OTHER INFORMATION: Xaa is any amino acid
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                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/09509814A; Patent No. 6376227
                                                                                                                                                     420 VPVSPQTFSLAIVH 433
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ORGANISM: Bacillus sp.
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                                                                                                                                                                                                   360 SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNWMDGRNNVENVFNAPQSGTYTVEVQARN 419
                                                                                                                                                                                                                           61 NANDPNGHGTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 119
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240 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKDSLLKAALIAGAADVGLGF 299
                                                                                                    300 PNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA 359
                                                                                                                                  507 PNGNQGWGRVTLDKSLVWSYVNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TAKAIWA, MIKIO
APPLICANT: TAKAIWA, MIKIO
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KAASUMISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: SHIKATA, SAUSHI
APPLICANT: SHIKATA, SAUSHI
APPLICANT: SHIKATA, SAUSHI
APPLICANT: NOWURA, MASAFUMI
TITLE OF INVENTION: ALKLINE PROTEASE
FILE REFERENCE: 0327-0922-0PCT
CURRENT APPLICATION NUMBER: PCT/JP98/04528
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: UP 9-274570
PRIOR APPLICATION NUMBER: UP 9-274570
PRIOR RILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09509814A
Patent No. 6376227
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    420 VPVSPQTFSLAIVH 433
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LENGTH: 639
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ä 179 360 SLILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 419 265 NANDPNGHGTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 119 385 445 505 300 PNGNÇGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA 359 299 120 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGFGSGTISAPGTAKNAI 180 TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF 386 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKFDVMAPGTXILSARSGLAPDSSF 240 WANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGF 1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN 1; Gaps DB 4; Length 639; Indels 91.5%; Score 2060.5; DB 4; 91.7%; Pred. No. 6.2e-159; ive 12; Mismatches 23; CCATION: (592)...(592)

COTHER INFORMATION: Xaa is any amino acid
MAME/KEY: misc_feature
LCCATION: (594)...(594)

COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: (595)...(595)

COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: (595)...(595)

COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: (596)...(596)

COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: (611)...(611)

COCATION: (612)...(612)

COCATION: (632)...(632)

COTHER INFORMATION: Xaa is any amino acid
US-09-509-814A-1 APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUW
APPLICANT: NOWURA, MASARUMI
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REPERENCE: 0327-0832-0PCT
CURRENT APPLICATION NUMBER: US/09/509,814A RESULT 6
US-09-509-814A-2
'S-09-509-814A-2
'Sequence 2, Application US/09509814A
'Patent No. 6376227 GENERAL INFORMATION:
APPLICANT: TAKAINA, MIKIO
APPLICANT: TAKUDA, MITSUVOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: KUBOTA, HIROMI
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHIKATA,
APPLICANT: SHIKATA, SHIKATA,
APPLICANT: NOWIRA, MASAFUMI ||| || || ||||||||||| VPVGPQXFSLAIVN 639 420 VPVSPOTFSLAIVH 433 Query Match
Best Local Similarity 91.7%;
Matches 398; Conservative NAME/KEY: misc_feature 626 61 q g ò 셤 ò d ઠે d ద g ò à g ò 8

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LOCATION: (166)(166) OTHER INFORMATION: Xaa i NAME/KEY: misc_feature	LOCATION: (173)(173) OTHER INFORMATION: Xaa i NAME/KEY: misc_feature	a x z	LOCATION: (188)(188) OTHER INFORMATION: Xaa i NAME/KEY: misc feature	LOCATION: (189)(189) OTHER INFORMATION: Xaa i	LOCATION: (190)(190) OTHER INFORMATION: Xag i NAME/KEY: misc feature	LOCATION: (195)(195) OTHER INFORMATION: Xaa i NAME/KEY: misc feature	LOCATION: (287)(287) OTHER INFORMATION: Xaa i NAME/KEY: misc feature	LOCATION: (307). (307) OTHER INFORMATION: Xaa i	LOCATION: (325)(325) OTHER INFORMATION: Xaa i	NAME/KEY: MISC FEACUTE LOCATION: (370)(370) OTHER INFORMATION: Xaa i	NAME/KEY: misc feature LOCATION: (432)(432) OTHER INFORMATION: Xaa i	NAME/KEY: misc feature LOCATION: (502)(502)	NAME/KEY: misc feature LOCATION: (532)(532)	OTHER INFORMATION: Xaa 1 NAME/KEY: misc feature	LOCATION: (542)(542) OTHER INFORMATION: Xaa i NAME/KEY: misc feature	LOCATION: (585)(585) OTHER INFORMATION: Xaa i	NAME/KEY: misc feature LOCATION: (592) OTHER INFORMATION: Xaa i	NAME/KEY: misc feature LOCATION: (593)(593)	OTHER INFORMATION: Xaa i NAME/KEY: misc feature 10CAMTON: (EGE) (EGE)	OTHER INFORMATION: Xaa i NAME/KEY: misc feature	(596)(596) ORMATION: Xaa	NAME/KEY: misc feature LOCATION: (597)(597)	XEY: misc feature	FORMATION: Xaa : misc feature	N: (633) (633) NFORMATION: Xaa 14A-2	Query Match Sest Local Similarity 91 Best Local Similarity 91
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241 ANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 LTLVNDLDLVITAPNGTKYYGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNV
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                                                                                                Query March 90.2%; Score 2032; DB 4; Length 4 Best Local Similarity 88.7%; Pred. No. 7.3e-157; Matches 384; Conservative 25; Mismatches 24; Indels
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                                                   STRAIN: Bacillus sp. Y
             MOLECULE TYPE: protein ORIGINAL SOURCE:
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linear
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                                                                    US-09-104-623A-4
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TOPOLOGY:
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APPLICANT: Patum, Tine Muxoll
APPLICANT: Detum, Tine Muxoll
APPLICANT: Detum, Tine Muxoll
APPLICANT: Detum, Erwin Lude
APPLICANT: Roggen, Erwin Lude
APPLICANT: Roggen, Erwin Lude
AUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 63037520 No. 6303752disk of No. 6303752th America, Inc.
GITY: New York
STRATE: NY
                                                                                                                                                                                                                                                                                                                                                    206
                                                                                                                                                                                                                                                                                                                                                                                       359
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                                                                                                                                                                 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 179
                                                                                                                                                                                              327 AGARIHTUSWGAAVNGAYTIDSRNVDDYVRKNDMTILFAAGNEXPNGGTISAFGTAKNAI 386
                                                                                                                                                                                                                                           TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF 239
                                                                                                                                                                                                                                                               387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKFDVMAPGTXILSARSSLAPDSSF 446
                                           267 NANDTNGHGTHVAGSVLGNGXTNKGMAPQANLVFQSIMDSXGGLGGLPSNLQTLFSQAXS 326
                     NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHBAFRGKITALYALGRTN 60
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,623A
FILING DATE: US/09/104,623A
FILING DATE: VINORMATION:
NAME: ROASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: ROASS, Carol
REGISTRATION NUMBER: 36,993
REFERRENCE/POCKET NUMBER: 5256.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09104623A Patent No. 6303752 GENERAL INFORMATION:
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TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: amino acid
STRANDEDNESS:
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ZIP: 101
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                                                                            GENERAL INFORMATION:
APPLICANT: Olsen, Anne Agerlin
APPLICANT: Prent, Annette
TITLE OF INVENTION: A Modified Enzyme for Skin Care
TITLE OF INVENTION: A Modified Enzyme for Skin Care
TITLE REPERENCE: 4922.204-US
CURRENT APPLICATION NUMBER: US/09/019,532B
CURRENT FILING DATE: 1996-02-05
EARLIER APPLICATION NUMBER: 0038/97
EARLIER PILING DATE: 1997-01-10
EARLIER PILING DATE: 1997-06-25
EARLIER PILING DATE: 1997-07-07
EARLIER PILING DATE: 1997-07-07
EARLIER PILING DATE: 1997-07-07
EARLIER PILING DATE: 1997-01-12
SALLIER PILING DATE: 1997-01-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FRAGERQ for Windows Version 3.0
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Best Local Similarity 88.7%; Pred. No. 7.3e-157;
Matches 384; Conservative 25; Mismatches 24;
Sequence 4, Application US/09019532B Patent No. 6416756
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203 NDVARGIVKADVAQNNYGLYGQGQLVAVADTGLDTGRNDSSWEBFRGKITALYALGRIN 262
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                                                                                                                                                                                                                                121 GARIHINSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAFGTAKNAIT 180
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                                         181 VGATENIRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW
                                                                        241 ANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
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Sequence 43, Application US/08873479
GENERAL INFORMATION:
APPLICANT: Sloma, Alan
APPLICANT: Lynne, Ghristianson
TILLE OF INVENTION: Mucleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCE: 57
NUMBER OF SEQUENCE: 57
ADDRESSEE: No. 58917010 No. 5891701th America
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OPERATING SYSTEM: DOS
SOCTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,479
FILING DATE: 12-UUN 1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: AFIS, Cheryl H
REGISTRATION NUMBER: 34,086
REBERNICH/OCKET NUMBER: 521.000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 405 Lexington Avenue
CITY: New York
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211.10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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amino acid
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Best Local Similarity 88.7
Matches 384; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acid
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US-08-873-479-43
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                                                                                                                NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 120
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                                                           61 NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA
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Sequence 4, Application US/09338746

Sequence 4, Application US/09338746

GENERAL INFORMATION:
APPLICANT: Described Heinz-Josef
APPLICANT: Discribed Heinz-Josef
APPLICANT: Fatum, Tine M.
TITLE OF INVENTION: A Polypeptide-Polymer Conjugate
TITLE OF INVENTION: A Polypeptide-Polymer Conjugate
TITLE OF INVENTION: A Polypeptide-Polymer Conjugate
CURRENT APPLICATION NUMBER: US/09/338,746
CURRENT FILING DATE: 1999-06-23

EARLIER APPLICATION NUMBER: PA 1998 00809

EARLIER APPLICATION NUMBER: 60/091,461

SARLIER FILING DATE: 1998-07-01

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FatISEQ for Windows Version 3.0

SEQ ID NO 4.
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88.7%; Pred. No. 7.3e-157;
tive 25; Mismatches 24;
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Best Local Similarity 88.77
Matches 384, Conservative
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RESULT 13
US-09-196-281-13
Sequence 13. Application US/09196281A
Sequence 13. Application US/09196281A
Sequence 13. Application US/09196281A
Settle No. 6605458
GENERAL INFORMATION:
APPLICANT: Hansen, Peter K.
APPLICANT: Badditz, Peter
APPLICANT: Mikkelsen, Frank
TITLE OF INVENTION: Procease Variants And Compositions
FILE REPERENCE: 3435.200-US
CURRENT APPLICATION NUMBER: 1332/97
EARLIER APPLICATION NUMBER: 1332/97
EARLIER APPLICATION NUMBER: 1332/97
SARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 13
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                     301 NGNQGWGRVTLDKSLNV
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                                                                                         GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT 180
                                                                                                                   323 GARIHTINSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT 382
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                            NANDPNCHCTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 120
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US-09-512-251A-10
US-09-512-251A-10
Sequence 10, Application US/09512251A
Fatent No. 655535
GENERAL INFORMATION
APPLICANT: Handers, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelsen, Frank
APPLICANT: Andersen, Kim
TITLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 2549-2049-US
CURRENT APPLICATION NUMBER: US/09/512,251A
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.2%; Score 1649; DB 4; L. Best Local Similarity 100.0%; Pred. No. 6.2e-126; Matches 317; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSGPORFSLAIVH 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVSPQTFSLAIVH 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-512-251A-10
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61 NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 NANDPNGHGTHVAGSVLGNATNKGNAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA
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73.2%; Score 1649; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.2e-126;
Matches 317; Conservative 0; Mismatches 0; Indels
US-09-515-150A-10

| Sequence 10, Application US/09515150A |
| Sequence 10, Application US/09515150A |
| Patent No. 6558938 |
| GENERAL INFORMATION: |
| APPLICANT: Hansen, Peter |
| APPLICANT: Andersen, Kim |
| APPLICANT: Andersen, Kim |
| APPLICANT: Andersen, Kim |
| APPLICANT: Andersen, Kim |
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| APPLICANT: Andersen, Kim |
| APPLICANT: Andersen, Kim |
| APPLICANT: Andersen, Kim |
| SEQUENCE: ANDERSENCE: A
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RESULT 15
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                                                                                                                                                                           1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 60
                                                                                                                                         0; Gaps
                                                                                              Query Match 73.2%; Score 1649; DB 4; Length 345; Best Local Similarity 100.0%; Pred. No. 6.2e-126; Matches 317; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08894818B
Patent No. 6261822
GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: MITTA, Masanori
APPLICANT: MITTA, Masanori
APPLICANT: ASABA, Kiyozo
APPLICANT: ASABA, Kiyozo
APPLICANT: TSUNSA, MASONORI
APPLICANT: TSUNSA, MASONORI
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATY APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington SCOMMENTED D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICR APPLICATION DATA.
APPLICATION NUMBER. PCT/JP96/03253
FILING DATE. 07.NOV-1996
PRICR APPLICATION DATA.
APPLICATION NUMBER. JP 323285/1995
FILING DATE. 12.DEC-1995
ATTOCNEY AGENT INFORMATION.
NAME: Browdy, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1998
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REGISTRATION NUMBER: 2
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; LENGTH: 345
; TYPE: PRT
; ORGANISM: Bacillus
US-09-196-281-13
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US-08-894-818B-1
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199 GHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKY 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 VGA-------VDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRAS---GTSMG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 TPINDYYTKASGISMATPHVSGVGALILQAH-----PSWTPDKVKTALIETADIVAP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 -----DVSGATFVTATLYWDTGSSDIDLYLYDPNGNE-VDXSYTAYY------GFEKV 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 GHGTHVAGSVLG----NATNKGMAPQANLVFQSIM--DSGGGLGGLPANLQTLFSQAYSA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAFDSSFW 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 SLVWSDAFGSTTASLTLV-----NDLDLVITAPNGTKYYGNDFTAPYDNNWDGRNNVENV 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: RATO, Ikunoshin
JITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REPERBICE: TAKAKURa-6
CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR FILING DATE: 1997-06-10
PRIOR FILING DATE: 1997-06-10
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
19.2%; Score 432.5; DB 3; Length 659;
Best Local Similarity 30.7%; Pred. No. 7.2e-27;
Matches 134; Conservative 62; Mismatches 156; Indels 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-445-472-12; Sequence 12, Application US/09445472; Patent No. 6358726
REFERENCE/DOCKET NUMBER: TAKG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
STRANDEDNESS: single
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506 GYYNPTAGTWTVKVVSY 522
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CRGANISM: Thermococcus celer
US-09-445-472-12
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                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide US-08-894-818B-1
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al Sin 134;	Matches 134; Conservative 62; Mismatches 156; Indels 85; Gaps	16;
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63	GHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA	120
199	GHĠTHVAĠIVAĠTGSVNSQYIĠVAPGAKLŸGVKVLGAĎGSĠSVSTIIAGVDWVVQNKDKX	258
121	GARIHTINSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSCTISAPGTAKNAIT	180
259	GIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAAASKVIT	318
181	VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKE	240
319	VGAVDSNDNIASFSSRGPTADG	364
241	ANHDSKYAYMGGISMATPIVAG-NVAQLREHFVKNRGVTPKPSLLKAALIAGA	292
365	TPINDYYTKASGTSMATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAP	416
293	ADVGLGFPNGNOGWGRVTLD	346
417	KEIADIAYGAGRVNVYKAIKYDDYAKLIFTGSVADKGSATHTF	459
347	SLVWSDAPGSTTASLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENV	401
460	DVSGATFVTATLYWDTGS	505
402	FINAPOSGTYTVEVQAY 418	
506		

Search completed: March 31, 2004, 16:11:57 Job time: 14.9892 secs

Foreign p Fragment

Protein e Streptomy

DhpA-mel

Aaw24122 Aaw94838 Aaw94838 Aaw24123 Aabb09483 Aabb09483 Aabb09483 Aabb09483 Aaw13668 Aaw13668 Aaw13668 Aaw1368 Aaw1368 Aaw24124 Aar87007 Aar87007 Aar87007 Aar87007 Aar87007 Aar87008

Hyperther

Protease

T. yonsei Transglut Hyperther Protease.

RP-III re Xanthomon

Streptomy Streptomy

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This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease Ya from Bacillus sp strain Y-(FERM BP-1029) described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified alkaline proteases useful in detergent compositions
                                                                                                                                                                                                                                                                                                                                Bacillus sp Y-(FERM BP-1029) alkaline protease protein fragment.
                                                                                                                                                                                                                                                                                                                                                    Alkaline protease; detergent; laundry; bleaching; dishwasher.
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100.0%; Score 2260; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.5e-169;
Matches 433; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                     ALIGNMENTS
                                               ABB09483
AAB81180
                                                                             AAW13666
                                                                                                          ABU11343
                                                                                                                                                                                                                                                                        AAM50083 standard; protein; 433 AA.
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12-APR-2001; 2001JP-00114048
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                                                                                                                                                                                                                                                                                                              12-AUG-2002 (first entry)
Hatada Y, Ogawa A,
Okuda M, Saeki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-437518/47.
(KAOS ) KAO CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 433 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     surface active agent resistance; detergency improver
                                                 NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA
                                                                                       121 GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKONALT
                                                                                                                              YILVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYNV
            NDVARGIVKADVAQNNYGLYGGGOVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                               NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA
                                                                       GARIHTINSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
                                                                                                                  VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
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Query Match
99.4%; Score 2247; DB 2; Length 433;
Best Local Similarity 99.3%; Pred. No. 5.7e-168;
Matches 430; Conservative 3; Mismatches 0; Indels
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N-PSDB; AAQ27516.
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/note= "The enzyme is modifed by methoxypolethyleneglycol
molecules covalently attached to the N-terminal amino
group and to fourteen unspecified amino groups of lysine
residues present on the surface of the enzyme"
                                                            120
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                                                                             181 VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
                  NDVARGIVKADVAQNNYGLYGQGQLVAVADTGLDTGRNDSSMHBAFRGKITALYALGRTN
                                                                                                                         GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
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NDVARGIVKADVAQNNYG1YGQQQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus lion Y protease; polyethylene glycol; PEG; soap;
methoxypolethyleneglycol; mPEG; skin; hair care product; cosmetic;
lipstick; hair gel; sun oil; shampoo; hair dye; insect repellant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New enzyme modified by attachment of many polymeric molecules
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The present sequence represents the Bacillus lion Y protease. The invention claims for enzymes covalently modified on their surface by the attendent of a large number of small polymeric molecules, e.g. polyechylene glycols (PEG). The polymeric molecules are coupled to the N-terminal amino group and the amino groups of lysine residues found on the surface of the enzyme. In the example given, the lion Y protease was modified using methoxypolethyleneglycol (MPEG) as the polymeric molecule. The N-terminal amino group and the amino groups of the fourteen lysine residues present on the surface of the lion Y protease were modified. Modification of the enzymes increases the stability and/or reduces the sensitising potential (allergenicity) of the enzyme, without significantly reducing enzymatic activity. Also, using a large number of relatively small polymeric molecules, rather than a few very large ones, provides a more even effect with reduced activity loss. The modified and hair care products, e.g. soaps, components of a wide range of skin and hair care products, e.g. soaps, cosmetics, creams, gels, libsticks, hair gels, sun oils, shampoos, hair dyes, insect repellants, etc
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skin and hair care products, has reduced tendency to cause sensitisation and increased stability.
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Pred. No. 5.7e-168;
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PD498; subtilisin; Lion Y; protease; skin-care; feed; additive; soap;

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                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of Lion Y protease. This can be used as an active ingredient: (1) in personal care products (especially skin-care products such as soaps, cosmetics, hair dyes, sunscreens, anti-acne products, antiperspirants, insect repellants or decodorants); (ii) in detergents (as laundry, dishwashing or hard-sunrface cleaners); (iii) food or feed addittives (e.g. for breadmaking); (iv) in textile-treating compositions, or (v) in oral or dermal pharmaceuticals and agrochemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
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cosmetic; hair dye; sunscreen; acne; antiperspirants; insect repellant; deodorant; detergent; food; breadmaking; textile-treating; oral; dermal; pharmaceutical; agrochemical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 NGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGDOGWGRVTLDKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GARIHTINSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHBAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NDVARGIVKADVAQNNYGLYGQGQLVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                   New modified polypeptide with attached low molecular weight polymer reduced respiratory allergenicity, useful in skin care products, detergents, as food additives or textile-treating compositions.
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Pred. No. 5.7e-168;
3; Mismatches 0;
                                                                                                                                                                                                                                                             Eľ.
                                                                                                                                                                                                                                                               Roggen
                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 48-49; 60pp; English
                                                                                                                                                                                                                                                             Deussen H,
                                                                                                                                                                                     97DK-000000753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.3%;
Matches 430; Conservative
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                                                                                                                                                                                                                                                               Fatum TM,
                                                                                                                                                                                                                                                                                            WPI; 1999-095735/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 433 AA;
                                                                                                                                                                                                     07-JUL-1997;
                                                                                            WO9900489-A1
                                                                                                                                                      22-JUN-1998;
                                                                                                                                                                                     25-JUN-1997;
                                                                                                                          07-JAN-1999
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241 ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP
                                                             361 YILVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYNV
                                             301 NGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS
                                                                                                   YTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYNV
                                                                                                                                                                                                                                                                                                                                                                          allergic response; industrial composition;
                                                                                                                                                                                                                                                                                                                                                                                    co-polymer; ethylene oxide; EO; propylene oxide; PO; conjugate; allergenicity; detergent; cosmetic; toiletries; textile treatment; agrochemical; pharmaceutical; food; feed additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.4%; Score 2247; DB 3;
99.3%; Pred. No. 5.7e-168;
iive 3; Mismatches 0;
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in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roggen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 56~57; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fatum TM,
                                                                                                                                                                                                                                                             AAY44619 standard; protein; 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98DK-00000809
                                                                                                                                                             PSGPQRFSLAIVH 433
                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                          Lion Y enzyme; protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                               Bacillus Lion Y enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olsen AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-136981/12.
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Best Local Similarity
Matches 430; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9967370-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus sp
                                                                                                                                                                                                                                                                                                                     07-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deussen H,
                                                                                                      361
                                                                                                                                                             421
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                                                                                                                                                                                                                                                                                        AAY44619;
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                                                                                                                                                                                                                                               AAY44619
ID AAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide-polymer conjugate, particularly enzyme conjugate, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gарв
                                                                                                                                                          Protease Lion Y; polypeptide-polymer conjugate; washing performance; respiratory allergenicity; allergic reaction; detergent formulation; laundry; dishwashing; hard surface cleaner; agricultural chemical; skin care; cosmetic; oral pharmaceutical; dental pharmaceutical; textile processing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 433;
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Pred. No. 5.7e-168;
                                                                                                                                                                                                                                                                                                                                                                                                                       Deussen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                Amino acid sequence of protease Lion Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 74-76; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Olsen AA,
                                             AAY69207 standard; protein; 433
                                                                                                                                                                                                                                                                                                                                   99WO-DK000406,
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                                                                                                                                                                                                                                                                                                                                                              98DK-00000951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detergent formulations.
                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                     Fatum TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-195024/17
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Best Local Similarity
Matches 430; Conserv
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                                                                                                                                                                                                                                                                          WO200004138-A1
                                                                                                                                                                                                                                                                                                                                   16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                             17-JUL-1998;
                                                                                                                                                                                                                                               Bacillus sp.
                                                                                                    30-MAY-2000
                                                                                                                                                                                                                                                                                                      27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                       Bauditz P,
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enzyme, with copolymer of e.g. cleaning compositions,
                                                                                                                                                                                                          The present sequence is a Bacillus Lion Y enzyme, which is a protease capable of inducing an allergic response upon inhalation. The enzyme c be covalently coupled to a co-polymer comprising ethylene oxide (EO) a propylene oxide (PO) to reduce its allergenicity. This enzymer conjugate can be used in industrial compositions such as detergents, cosmetics, toiletries, textile treatment compositions, agrochemicals, oral and dermal pharmaceuticals and food and feed additives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NDVARGIVKADVAQNNYGLYGQGQLVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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                                                                                     VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW 240
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 NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $(34 - 33$) compared to prior art alkaline proteases (31 and 23$). This sequence represents a fragment of the alkaline protease SD-521 from Bacillus sp strain SD-521 (FERM BP-11162) described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel Bacillus sp. alkaline proteases useful in
                                    GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
                                                                 VGATENYRPSFGSIADNPNHIAOFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
                                                                                                             ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP
                                                                                                                                                                                                                                                                                                                                                                                           (FERM BP-11162) alkaline protease protein fragment
                      GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
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                                                                                                                                                                                                                                                                                                                                                                                                                 detergent; laundry; bleaching; dishwasher
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Pred. No. 2e-167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified alkaline proteases useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato
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12-APR-2001; 2001JP-00114048.
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Saeki K;
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                                                                                                                                                                                                                                                                                                                                                                                             SD-521
                                                                                                                                                                                                                                                                                                                                                                                                                  Alkaline protease;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                         NGDOGWGRVTLNKSLNVAYVNEATALATGOKATYSFOAQAGKPLKISLVWTDAPGSTTAS
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                                                                                                                         61 NANDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA
                                                                                                                                                            GARIHTINSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAFGTAKNAIT
                                                                                                                                                                                      121 GARIHTNSWGAPVNGAYTANSROVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
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                                                                                              NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFOSIMDSSGGLGGLPSNLNTLFSQAMNA
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                              1 NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alkaline protease Y; detergent; surfactant; leather processing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel protease from Bacillus subtilis LC20 - useful dishwashing detergents and for leather processing.
 1;
 Mismatches
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                    production of such proteases. The protease are used in laundry and dishwashing detergents, for institutional and industrial cleaning, and dishwashing detergents, for institutional and industrial cleaning, and dishwashing, as well as for debittering and enhancing the degree of hydrolysis of protein hydrolysates, for flavour development enrough hydrolysis of proteins, degradation of undesired peptides and in erzymatic synthesis of peptides. They have enhanced stability towards oxidation under alkaline conditions, e.g. towards bleaching agents of the protease activity is diminished. Such cells an he used for the production of heterologous recombinant proteins
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                                                                                                                                                                                                                                                                                                                                               1; Indels
  recombinant host cells and methods for the
                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                 Score 2238; DB 2
Pred. No. 5e-167;
3; Mismatches
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.1%;
Matches 429; Conservative
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                                                                                                                                                                                                                                                            Sequence 636 AA;
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detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (14 - 18%) compared to prior art alkaline proteases (11 and 21%). This sequence represents a fragment of the alkaline protease B-1 from Bacillus sp strain D6-(BERM-P1592) described in the method of the invention
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                                                                                                                                                                                                                                                                                                                          New modified alkaline proteases useful in detergent compositions
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                                                                                         Sumitomo
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Best Local Similarity 98.6%; Pred. No. 6e-167;
Matches 427; Conservative 3; Mismatches 3;
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                                                                                         Kageyama
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                                                                                    Ogawa A,
Saeki K;
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(KAOS ) KAO CORP
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This is the amino acid sequence of a novel protease of Bacillus sp. JP170 (NCIB 12513), as deduced from the nucleotide sequence of an isolated gene (see AAW82382). The entire protein, including the signal peptide and protein, and protein, including the signal peptide and protein and protein and protein protein are combinant production of the protease Y (see AAW89548) (from Bacillus. The invention provides vectors, recombinant host cells and methods for the recombinant production of the protease is used in laundry and dishwashing deergants, for institutional and industrial cleaning, and for leather processing, as well as for debittering and enhancing the degree of hydrolysis of proteins, degradation of undesired peptides and in enzymatic synthesis of proteins, that as enhanced stability towards oxidation under alkaline conditions, it has enhanced stability towards oxidation under alkaline conditions, provides mutant cells in which the protease activity is diminished. Such cells can be used for the protease activity is diminished. Such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 nbvargivkabvagnneglyggggjvavabiglbigrnbssmeafrgkifalyalgrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel protease from Bacillus subtilis LC20 - useful in laundry and dishwashing detergents and for leather processing.
                           Protease; detergent; surfactant; leather processing; debittering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%; Score 2033; DB 2;
88.7%; Pred. No. 6.5e-151;
live 25; Mismatches 24;
                                                                                                                                                                       /note= "prepro region"
209. .641
/note= "mature protein"
                                                                                                                         . .33
note= "signal peptide'
                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 53-54; 77pp; English
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Best Local Similarity 88.77
Matches 384; Conservative
                                                                                                                                                        .208
Bacillus JP170 protease
                                                                                                                                                                                                                                                                                                                                                                                                Christianson
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-080908/07.
N-PSDB; AAV82382.
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                                                                                                                                                                                                                                                                                                      39-JUN-1998;
                                                                                                                                                                                                                                                                                                                                     12-JUN-1997;
                                                                              Sp.
                                                                                                                                                                                                                                                                     17-DEC-1998,
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                                                                                                                                                                                                                                                                                                                                                                                                      Sloma A,
                                                                           Bacillus
                                                                                                             Key
Peptide
                                              flavour
                                                                                                                                                                                          Protein
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                                                                                                                                                                                                                                                                                                  This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38$) compared to prior art alkaline proteases (31 and 23$). This sequence represents a fragment of the alkaline protease A-2 from Bacillus sp NCIB12513 described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT 180
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                                                                                                                                                                                                                                        New modified alkaline proteases useful in detergent compositions
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                                                                                                                                                             Sumitomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 433;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Score 2033; DB 5; 88.7%; Pred. No. 3.8e-151; ive 25; Mismatches 24;
                                                                                                                                                           Araki
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                                                                                                                                                             Sato
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                                                                                                                                                             Kageyama
                                               22-NOV-2001; 2001EP-00127851.
                                                                              22-NOV-2000; 2000JP-00355166.
12-APR-2001; 2001JP-00114048.
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Saeki K,
                                                                                                                                                                                                         WPI; 2002-437518/47.
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Best Local Similarity
                                                                                                                            (KAOS ) KAO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 433 AA;
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                  29-MAY-2002
                                                                                                                                                           Hatada Y,
Okuɗa M,
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Length 641; Indels

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This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease KP9860 from Bacillus sp strain KSM-KP9860 described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
181 TVGATENIRPSFGSYADNINHVAOFSSRGPTKDGRIKKPDVMAPGTFILSARSSLAPDSSF
                                                                                                               PNGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTA
                                                                                                                                                                     361 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNWHGRNNVENVFINAPQSGTYTVEVQAXN
                                           TVGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSF
                                                                                               240 WANYNSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGY
                                                                                                                                                                                                        SYTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIBVQAYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alkaline protease; detergent; laundry; bleaching; dishwasher.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus ap KSM-KP9860 alkaline protease protein fragment.
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88.5%; Score 1999.5; DB 5; Length
Best Local Similarity 88.0%; Pred. No. 1.6e-148;
Matches 382; Conservative 27; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                           AAM50081 standard; protein; 434
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12-APR-2001; 2001JP-00114048
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Saeki K;
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Okuda M,
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                                                                                                             361 YILVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIJEVQAYNV 420
                                                                                                                                       628
     ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP 300
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                        449 ANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
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                                                                                                                                                                                                                                                                                                                                                                          Alkaline protease; detergent; laundry; bleaching; dishwasher.
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                                                                                                                                                                                                                                                                                                                                              Bacillus sp alkaline protease protein A-1 fragment.
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12-APR-2001; 2001JP-00114048
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Best Local Similarity 87.6%
Matches 380; Conservative
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Saeki K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVILVNDLDLVITAPNGTRXVGNDFSAPFDNNWDGRNNVENVFINSPQSGTYTIEVQAYN 420
                                       NASDPNGHGTHVAGSVLGN-ALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWN 119
                                                                                                                                                                                                                                                                       WANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGY 299
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                                                                                                                                                   AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
                                                                          NANDTNGHGTHVAGSVLGNGATNKGMAPQANLVFQSIMDSSGGLGGLPSNLQTLFSQAFS
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  NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                  AGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protease; Bacillus; casein digestion; oleic acid; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kageyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hitomi J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPSGPORFSLAIVH 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPVGPQNFSLAIVN 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus alkaline protease
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(first entry)
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composition, oxidising agent.
                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                      88.1%; Score 1991.5; DB 2; 87.8%; Pred. No. 1.2e-147; ive 27; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640 AA
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                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.8
Matches 381; Conservative
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Kageyama Y;

Hitomi J,

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The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by oleic acid and they have a high stability to oxidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 6-11; (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the bleaches. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.)
                                                                                                                                               Alkali protease from Bacillus used in washing powders.
                    Saeki K, Kubota H,
                                                                                                                                                                                           Disclosure; Page 63-68; 71pp; Japanese
                  Okuda M,
Nomura M;
                                                                                   WPI; 1999-287736/27.
                                                                                                        N-PSDB; AAX37279
                    Takaiwa M,
Shikata S,
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Sequence 640 AA

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266
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                                                                                                                                                                                                                                                                                                                                          327 AGARIHTINSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
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                                                                                                                                                                                                                                                         267 NANDINGHGTHVAGSVIGNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
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                                                                                                       1 NDVARGIVKADVAQNNYGLYGQGQVVAVAVATGLDTGRNDSSMHBAFRGKITALYALGRTN 60
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                                                      Gaps
                                                      Ξ,
Query Match

88.0%; Score 1988.5; DB 2; Length 640;

Best Local Similarity 87.3%; Pred. No. 2e-147;

Matches 379; Conservative 29; Mismatches 25; Indels 1;
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99.4%; Score 2247; DB 4; Length 433;
Best Local Similarity 99.3%; Pred. No. 4.4e-169;
Matches 430; Conservative 3; Mismatches 0; Indels
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MEDIUM TYPE: Diskette
COMPUTER IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM FORM:
APPLICATION DATA:
APPLICATION ATA:
APPLICATION ATA:
APPLICATION: 435
FILING DATE: 25-TUN-1998
CLASSIFICATION: 435
ATTORNEY, AGENT INPORMATION:
NAME: ROZEK, CARO]
REGISTRATION NUMBER: 5256.200-US
REFERENCE/DOCKET NUMBER: 5256.200-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
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US-08-332-677A-10
US-08-140-083A-10
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US-08-185-502-5
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Patent No. 6303752
GENERAL INFORMATION:
APPLICANT: Olsen, Arne Agerlin
APPLICANT: Fatum, Tine Muxoll
APPLICANT: Peussen, Heinz-Josef
APPLICANT: Roggen, Erwin Ludo
TITLE OF INVENTION: A Modified Polypeptide
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    US-09-024-532-3
US-08-269-050-4
US-08-090-207-1
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TYPE: amino acid
STRANDEDNESS:
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Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 11, Appl
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                                                                                                     March 31, 2004, 15:59:39; Search time 13.9892 Seconds (without alignments) 1597.947 Million cell updates/sec
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1 NDVARGIVKADVAQNNYGLY.......EVQAYNVPSGPQRFSLAIVH 433
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2. /GgTZ = 6/ptodata/2/iaa/5B COMB.pep:*

3. /GgTZ = 6/ptodata/2/iaa/6A COMB.pep:*

4. /GgTZ = 6/ptodata/2/iaa/6E COMB.pep:*

5. /GgTZ = 6/ptodata/2/iaa/PCTUS COMB.pep:*

5. /GGTZ = 6/ptodata/2/iaa/PCTUS COMB.pep:*

6. /GGTZ = 6/ptodata/2/iaa/PGTUS COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-509-814A-1

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US-08-94-1168-1

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Maximum Match 100%
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99.4%; Score 2247; DB 4;
Best Local Similarity 99.3%; Pred. No. 4.4e-169;
Matches 430; Conservative 3; Mismatches 0;
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Patent No. 6638526

GENERAL INFORMATION:
APPLICANT: Deussen, Heinz-Josef
APPLICANT: Deussen, Heinz-Josef
APPLICANT: Deussen, Heinz-Josef
APPLICANT: Parum, Tine M.
APPLICANT: Roggen, Erwin L.
TITLE OF INVENTION: A Polypeptide-Polymer Con
FILE REFERENCE: 5619-200-US
CURRENT APPLICATION NUMBER: US/09/338,746
CURRENT FILING DATE: 1999-06-23
EARLIER APPLICATION NUMBER: 60/091,461
EARLIER FILING DATE: 1988-06-23
EARLIER FILING DATE: 1988-06-3
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; ORGANISM: Bacillus
US-09-338-746-4
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99.4%; Score 2247; DB 4;
Best Local Similarity 99.3%; Pred. No. 4.4e-169;
Matches 430; Conservative 3; Mismatches 0;
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APPLICANT: Prent, Annette
TITLE OF INVENTION: A Modified Enzyme for Skir
TITLE OF INVENTION: A Modified Enzyme for Skir
TITLE OF INVENTION: A Modified Enzyme for Skir
CURRENT APPLICATION NUMBER: US/09/019,532B
CURRENT FILING DATE: 1996-02-05
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 0754/97
EARLIER APPLICATION NUMBER: 60/051,381
EARLIER APPLICATION NUMBER: 60/051,381
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1998-01-12
NUMBER OF SEQ ID NOS: 5
COFTWARE: FASCEGO for Windows Version 3.0
SEQ ID NO 4
SEQ ID NO 4
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ORGANISM: Bacillus sp.
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241 ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP 300
                                                         443 ANYNSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP
                                                                                                                                           SO3 SGDQGWGRVTLDKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS
                                                                                                                                                                                                                             563 YTLVNDLDLVITAPNGQXYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAXNV
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                                                                                                                                                                                                     361 YILVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYNV
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                                                                                                                 NGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42, Application US/08873479
Patent No. 5891701
GENERAL INFORMATION
APPLICANT: 510ma, Alan
APPLICANT: Lynne, Christianson
TITLE OF INVENTION: Nacleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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88.7%; Pred. No. 5.5e-152;
iive 25; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPUTED:
COMPUTER: IBM COMPUTED:
COPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: WANNERS: US/08/873,479
FILING DATE: 12-JUN-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: AGYIS, Cheryl H
REGISTRATION NUMBER: 34,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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                                                                                                                                                                                                                                                                                                421 PSGPORFSLAIVH 433
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Matches 384, Conservative
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MEDIUM TYPE: Diskette
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INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: si
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FRAGMENT TYPE:
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US-08-873-479-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGFNSGTISAFGTAKNAIT 382
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SGDQGWGRVTLDKSLNVAYVNBATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS 360
                                                                                                  361 YILVNDLDLVITAPNGQKYVGNDFSYPYDNWADGRNNVENVFINAPQSGTYIIEVQAYNV 420
                                                                     YILVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYNV 420
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99.4%; Score 2247; DB 2; Length 635;
Best Local Similarity 99.3%; Pred. No. 7.5e-169;
Matches 430; Conservative 3; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sloma, Alan APPLICANT: Sloma, Christianson TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide TITLE OF INVENTION: Having Protease Activity NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY OSA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketer
COMPUTER: DESCRIPTION
SYSTEM: DOS
SOFTWARE: PSASEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,479
FILING DATE: 12 JUN-1997
CLASSIFICATION: 530
ATTORNEY/AGRYT INFORMATION:
NAME: AGI'S. Cheryl H
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 5251.000-US
TELERHONE: 212-867-0123
TELERHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                    ; Sequence 43, Application US/08873479 ; Patent No. 5891701
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SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                              PSGPQRFSLAIVH 433
                                                                                                                                                                                                       421 PSGPORFSLAIVH 433
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linear
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61 NASDPNGHGTHVAGSVIGN-ALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWN 119
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386 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTYILSARSSLAPDSSF 445
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                                                                                                                                                                                                    360 SYTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYN
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                                                                            446 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVGLGY
                                                                                                                       300 PNGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTA
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                                            240 WANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGY
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Best Local Similarity 87.3%; Pred. No. 1.7e-148;
Matches 379; Conservative 29; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: RAGEXAMA, YABUSHI
APPLICANT: SHIKATA, SHITSUW
APPLICANT: SHIKATA, SHITSUW
APPLICANT: NOWRA, MASAFUMI
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REPERENCE: 0327-0812-0PCT
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: PCT/JP98/04528
PRIOR APPLICATION NUMBER: JP97-06-08
PRIOR APPLICATION NUMBER: JP97-06-08
NUMBER: OF SEQ ID NOS: 24
SEQ ID NOS: 24
SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09509814A
Patent No. 6376227
GENERAL INFORMATION:
APPLICANT: TAKAINA, MIXIO
APPLICANT: SAEXI, KATSUHISA
APPLICANT: SAEXI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HIROMI, JUN
                                                                                                                                                                                                                                                                                   VPSGPORFSLAIVH 433
                                                                                                                                                                                                                                                                                                                       626 VPVGPONFSLAIVN 639
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CRGANISM: Bacillus Sp.
US-09-509-814A-8
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                                                                                                      VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW 240
                                                                                                                             ANYNSKYAYMGGISMAIPIVAGNVAQLREHFIKNRGIIPKPSLIKAALIAGAIDVGLGYP 300
                                                                                                                                                                                                          NGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS 360
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                                                   GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIKIO
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBCA, HIROMI
APPLICANT: HIROMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: SHIKATA, SHITSUM
APPLICANT: SHIKATA, SHITSUM
APPLICANT: SHIKATA, SHITSUM
APPLICANT: SHIKATA, SHITSUM
APPLICANT: MAGSINAM
APPLICANT: MAGSARUMI
TITLE OF INVANTION: ALKALINE PROTEASE
FILE REPERENCE: 0327-0832-0PCT
CURRENT APPLICATION NUMBER: US/09/509, 814A
CURRENT FILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VESION 3.0
SENGTH: 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09509814A
Patent No. 6376227
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ORGANISM: Bacillus sp.
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GENERAL INVOCATION:
APPLICANT: TAKANA, MIKIO
APPLICANT: GRUDA, MITSTYCKHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: GRUDA, MITSTYCKHI
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: SHIKATA, SHITSUM
APPLICANT: SHIKATA, SHITSUM
APPLICANT: SHIKATA, SHIKALINE PROTEASE
FILE REFERENCE: 0327-0632-0PCT
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT FILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1997-66-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VERSION 3.0
SENGTHA: 639
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OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: (89)...(89)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: (102)...(102)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: (105)...(105)
OTHER INFORMATION: Xaa is any amino acid
OTHER INFORMATION: Xaa is any amino acid
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (23). (23)
LOCATION: (23). (23)
NAME/KEY: misc_feature
LOCATION: (29). (29)
LOCATION: (29). (29)
LOCATION: (29). (29)
NAME/KEY: misc_feature
LOCATION: (23). (23)
NAME/KEY: misc_feature
LOCATION: (32). (32)
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
NAME/KEY: misc_feature
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OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (47)...(47)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (53)...(53)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
NAME/KEY: misc_feature
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LOCATION: (128)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (130) .. (130)
OTHER INFORMATION: Xaa is any amino acid
OTHER INFORMATION: Xaa is any amino acid
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OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                              ; Sequence 1, Application US/09509814A; Patent No. 6376227; GENERAL INFORMATION:
420 VPSGPQRFSLAIVH 433
                                           627 UPVGPOTFSLAIVN 640
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SYTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYN 419
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Best Local Similarity 87.3%; Pred. No. 2.1e-148;
Matches 379; Conservative 29; Mismatches 25; Indels 1;
                                                                                                                                                                                                                                                                                                                                              us-uy-bu9-814A-6

sequence 6, Application US/09509814A

patent No. 634621.

GENERAL INPORMATION:

APPLICANT: TAKATWA, MITSUYOSHI

APPLICANT: MITSUYOSHI

APPLICANT: HITSUY, ARTSUHISA

APPLICANT: HITSUY, ARSUSHI

APPLICANT: HITSUY, ARSIGNERA

APPLICANT: SHIKATA, SHITSUW

APPLICANT: SHIKATA, SHITSUW

APPLICANT: SHIKATA, SHITSUW

APPLICANT: SHIKATA, SHITSUW

APPLICANT: NUNURA, YASUSHI

APPLICANT: NUNURA, WASHEWI

TITLE OF INVENTION: ALKALINE PROFTER

FILE REFERENCE: 0327-0832-0PCT

CURRENT FILING DATE: 1998-10-07

PRIOR APPLICATION NUMBER: 27

PRIOR APPLICATION NUMBER: 27

PRIOR APPLICATION NUMBER: 27

NUMBER OF SEQ ID NOS: 24

SOFIWARE: Patentin version 3.0

LENGTH: 640

"TWENT THE
                                                                                                                                                                                          420 VPSGPORFSLAIVH 433
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; ORGANISM: Bacillus sp.
US-09-509-814A-6
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LOCATION: (131)(131) OTHER INFORMATION: Xaa NAME/KEY: misc_feature	LOCATION: (132)(132) OTHER INFORMATION: Xaa NAME/KEY: misc_feature	LOCATION: (133)(133) OTHER INFORMATION: Xaa NAME/KEY: misc_feature	LOCATION: (146)(146) OTHER INFORMATION: Xaa NAMEKEY: MISC feature	OTHER INFORMATION: Xaa	LOCATION: (160)(160) OTHER INFORMATION: Xaa NAME/KEY: misc feature	LOCATION: (165)(165) OTHER INFORMATION: Xaa NAME/KEY: misc feature	LOCATION: (172)(172) OTHER INFORMATION: Xaa NAME/KEY: misc feature	LOCATION: (183). (183) OTHER INFORMATION: Xaa	LOCATION: (187)(187) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (188)(188)	NAME/KEY: misc feature LOCATION: (189)	OTHER INFORMATION: Xaa NAME/KEY: misc feature	LOCATION: (194)(194) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (286)	Olher Information: Add NAME/KEY: misc feature LOCATION: (306) (306)	OTHER INFORMATION: Xaa NAME/KEY: misc feature	LOCATION: (324). (324) OTHER INFORMATION: Xaa	NAME/KEI: WISC LEGIUTE LOCATION: (369)(369) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (431)(431)	OTHER INFORMATION: Xaa NAME/KEY: misc feature	LOCATION: (501)(501) OTHER INFORMATION: Xaa NAME/KEY: misc feature	LOCATION: (531)(531) OTHER INFORMATION: Xaa			misc react (591)(59 DRMATION: X	MAY: misc leatu ION: (592)(59 INFORMATION: X KEY: misc featu	rion: (594)(59

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                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NASDPNGHGTHVAGSVLGN-ALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 AGARIHTINSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAI 179
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                                                                                                                                                                                                                                                                                    Query Match 85.9%; Score 1941.5; DB 4; Length 639; Best Local Similarity 86.2%; Pred. No. 8.8e-145; Matches 374; Conservative 21; Mismatches 38; Indels 1;
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Patent No. 637627

GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIXIO
APPLICANT: SAEKI, KATSUHISA
APPLICANT: SAEKI, KATSUHISA
APPLICANT: SAEKI, KATSUHISA
APPLICANT: HITOMI, UUN
APPLICANT: HITOMI, UUN
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUW
APPLICANT: SHIKATA, SHITSUW
APPLICANT: SHIKATA, SHITSUW
APPLICANT: ONOUTA, MASAFUNI
TILLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0327-0832-0PCT
CURRENT FILING DATE: 2000-04-06
PRIOR FILING DATE: 2998-10-07
PRIOR FILING DATE: 1999-06-08
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (5957. (595)
OTHER INFORMATION: Xaa
NAME/KEY: misc feature
LOCATION: (596). (596)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (596). (596)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (611). (611)
OTHER INFORMATION: Xaa is any amino acid
LOCATION: (632). (632)
OTHER INFORMATION: Xaa is any amino acid
OTHER INFORMATION: Xaa is any amino acid
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